

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

(without alignments)
15094.505 Million cell updates/sec

Title: US-09-966-881-13

Sequence: 1 TGTTCCTCCTTCGATCACA.....TCCCCTTCTCCTATGATNG 806

Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	0%
	Maximum Match	100%

Listing first 45 summaries

Database

1:	gb_ba:	*
2:	gb_hlg:	*
3:	gb_in:	*
4:	gb_om:	*
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8:	gb_pl:	*
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13:	gd_un:	*
14:	gb_vl:	*
15:	em_ba:	*
16:	em_fun:	*
17:	em_hum:	*
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19:	em_mu:	*
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22:	em_ov:	*
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24:	em_ph:	*
25:	em_pl:	*
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27:	em_sts:	*
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29:	em_vl:	*
30:	em_hlg_hum:	*
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32:	em_hlg_other:	*
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36:	em_hlg_mam:	*
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41:	em_higo_other:	*

Pred. No. is the number of results predicted by chance to have a

Result		Query				Description	
No	Score	Match	Length	DB	ID		
1	778	96.5	806	6	A70152	A70152 Sequence 13	
2	612.4	76.0	1788	8	AF206320	AF206320 Musa acum	
3	591.8	73.4	748	6	AB3011	AB3011 Sequence 18	
4	591.8	73.3	745	6	AB3004	AB3004 Sequence 11	
5	588.8	73.1	793	6	AB3001	AB3001 Sequence 8	
6	588.8	73.1	793	6	MA299965	MA299965 Musa acum	
7	572.2	71.0	727	6	AB3014	AB3014 Sequence 21	
8	543.8	67.5	727	6	A70155	A70155 Sequence 16	
9	536	66.5	724	6	A70157	A70157 Sequence 18	
10	510.8	63.4	704	6	AB3002	AB3002 Sequence 7	
11	496.8	61.6	706	6	AB3012	AB3012 Sequence 19	
C 12	174.4	21.6	127202	2	CSJN00272	AT731627 Oryza sat	
C 13	169.4	21.0	1633	8	AY085026	AY085026 Arabidops	
C 14	152	18.9	90142	8	ATAC016827	ATAC016827 Arabidops	
15	151	18.7	823	6	AB3003	AB3003 Sequence 10	
16	150	18.6	1408	8	FX063550	FX063550 Fragaria x	
17	148	18.4	1523	8	AY086099	AY086099 Arabidops	
18	144.8	18.0	1496	8	AF206319	AF206319 Musa acum	
19	144.4	17.9	749	6	AB2999	AB2999 Sequence 6	
20	143.2	17.8	1462	8	MAPEL	X52943 M. acuminata	
21	142.8	17.7	842	6	A70156	A70156 Sequence 17	
22	141.4	17.5	708	6	AB3002	AB3002 Sequence 9	
23	141	17.5	1525	8	AY050404	AY050404 Arabidops	
24	141	17.5	1556	8	AY050795	AY050795 Arabidops	
25	134.6	16.7	687	6	A70153	A70153 Sequence 14	
26	134.6	16.7	687	8	MA299977	Z99977 Musa acumin	
27	133.2	16.5	5368	8	AF339024	AF339024 Fragaria	
28	131.6	16.3	772	6	AB3010	AB3010 Sequence 17	
29	131.6	16.3	772	8	MA299970	Z99970 Musa acumin	
30	131	16.3	758	6	AB3005	AB3005 Sequence 12	
31	130.4	16.2	1431	8	AY058197	AY058197 Arabidops	
32	129.2	16.0	794	6	AB3006	AB3006 Sequence 13	
33	128.8	16.0	728	6	AB3013	AB3013 Sequence 20	
34	128.4	15.9	745	6	AB3008	AB3008 Sequence 15	
35	127.2	15.8	1782	8	AY087724	AY087724 Arabidops	
36	127	15.8	1065	8	AY066033	AY066033 Arabidops	
37	127	15.8	1459	8	AY065034	AY065034 Arabidops	
38	127	15.8	1788	8	AY054200	AY054200 Arabidops	
39	126.2	15.7	731	6	AB3009	AB3009 Sequence 16	
40	124	15.4	1440	6	AX005936	AX005936 Sequence	
41	124	15.4	1440	8	ZEPCLY	Y09541 Z. elegans m	
42	123.6	15.3	4143	8	AF339025	AF339025 Fragaria	
43	122.6	15.2	100079	8	TT1G11	AC000276 Sequence	
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ALIGNMENTS

RESULT 1				
A70152				
LOCUS	A70152	806 bp	DNA	linear
DEFINITION	Sequence 13 from Patent WO9811228.			
ACCESSION	A70152			
VERSION	A70152.1	GI:4774567		
KEYWORDS	unidentified.			
SOURCE	unidentified			
ORGANISM	unclassified.			
REFERENCE	1 (Bases 1 to 806)			
AUTHORS	Seymour G.B., Bird C.R. and Medina-Suarez, R.D.			
TITLE	GENETIC CONTROL OF FRUIT RIPENING			
JOURNAL	Patent: WO 9811228 A 13 19-Mar-1998;			
	SEYMOUR GRAHAM BARRON (GB)			

FEATURES
source Location/Qualifiers
1. 806
/organism="unidentified"
/db_xref="taxon:32644"
/clone="U-068"

BASE COUNT 157 a 229 c 212 g 180 t 28 others
ORIGIN

Query Match 96.5%; Score 778; DB 6; Length 806;
Best Local Similarity 100.0%; Pred. No. 3.8e-193;
Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 60
DB 1 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 60
QY 61 GCATGACGGGGGTTTAAGATGATCCCTCTGCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 GCATGACGGGGGTTTAAGATGATCCCTCTGCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CTGGTTTGAACGAGGTCGGGGGTGATTGGAAGAGAGTCTCTGCTCGAGGAAT 180
DB 121 CTGGTTTGAACGAGGTCGGGGGTGATTGGAAGAGAGTCTCTGCTCGAGGAAT 180
QY 181 GCGGAGCATCGCGGAGGACCTTGAGAGAGGCTCCGCGAACCAGCCAGCGCATGCT 240
DB 181 GCGGAGCATCGCGGAGGACCTTGAGAGAGGCTCCGCGAACCAGCCAGCGCATGCT 240
QY 241 TCCTTGAAGAGGGCTGTAAACCCGGGAGAGACCCGAGTCGACGACCCGAGAG 300
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QY 301 GTTGCTTCGAGGTCCTGATGACCATATATCAACAGCAGGCTCGACATCTCTGTTAT 360
DB 301 GTTGCTTCGAGGTCCTGATGACCATATATCAACAGCAGGCTCGACATCTCTGTTAT 360
QY 361 CTGCTGCGGCTTACGCAACCCGATGACGACTGCTGGCGGTGCGACCTGATTGCGAT 420
DB 361 CTGCTGCGGCTTACGCAACCCGATGACGACTGCTGGCGGTGCGACCTGATTGCGAT 420
QY 421 GTCAACGAAAAAGCTCGCTGACTGCGGATGGCTTTGGAGCAACGNAATANGTGGC 480
DB 421 GTCAACGAAAAAGCTCGCTGACTGCGGATGGCTTTGGAGCAACGNAATANGTGGC 480
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QY 661 CGATGACNCGTGTCTCTGTCACATTTGCAATGGCCCTGCTCACCACCAATTTTCN 720
DB 661 CGATGACNCGTGTCTCTGTCACATTTGCAATGGCCCTGCTCACCACCAATTTTCN 720
QY 721 TCCCAACAACTCTTCTCANTNGCTCNCCTCCCAATGCAACCCGCGAATTTCTNGT 780
DB 721 TCCCAACAACTCTTCTCANTNGCTCNCCTCCCAATGCAACCCGCGAATTTCTNGT 780
QY 781 CCCCNCCTCCCTCTCTCTATGATNG 806
DB 781 CCCCNCCTCCCTCTCTCTATGATNG 806

RESULT 2
AF206320 1788 bp mRNA linear PLN 21-DEC-1999
LOCUS
DEFINITION Musa acuminata pectate lyase 2 (PL2) mRNA, complete cds.

ACCESSION AF206320
VERSION AF206320.1 GI:6606533
KEYWORDS
SOURCE Musa acuminata.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.

REFERENCE 1 (bases 1 to 1788)
AUTHORS Ong,C.K., Pua,E.C. and Liu,P.
TITLE Molecular cloning and characterization of pectate lyase in banana
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1788)
AUTHORS Ong,C.K., Pua,E.C. and Liu,P.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-1999) Department of Biological Sciences, National
University of Singapore, 10 Kent Ridge Crescent, Singapore 119260

FEATURES
source Location/Qualifiers
1. 1788
/organism="Musa acuminata"
/culturvar="Williams"
/db_xref="taxon:4641"
1. 1788
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NVTIIGHIHDCKPTGNAMVRSRSHGMRMTMDGAVSIFGSSHIMVHDCISLNCAD
GLVDAYVNGSTATTIVSNNTFTHHNEMLGHTDSYARSDINQVTFARHREBGLIQR
RCHRGYFHVNVNDYTHWEMTATIGSAPPTINSQGNRYLAPNPFPAEVRVPTDOST
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GTRC"

BASE COUNT 419 a 473 c 470 g 426 t
ORIGIN

Query Match 76.0%; Score 612.4; DB 8; Length 1788;
Best Local Similarity 88.6%; Pred. No. 1e-149;
Matches 716; Conservative 0; Mismatches 82; Indels 10; Gaps 6;

QY 1 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 60
DB 1 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 60
QY 15 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 74
DB 15 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 74
QY 61 GCATGACGGCGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 GCATGACGGCGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 75 GCATGACGGCGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 134
DB 75 GCATGACGGCGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 134
QY 121 CTGGTTTGAACGAGGTCGGGGGTGATTGGAAGCAAGTCTCTGCTCGAGGAAT 180
DB 121 CTGGTTTGAACGAGGTCGGGGGTGATTGGAAGCAAGTCTCTGCTCGAGGAAT 180
QY 135 CTGGTTTGAACGAGGTCGGGGGTGATTGGAAGCAAGTCTCTGCTCGAGGAAT 194
DB 135 CTGGTTTGAACGAGGTCGGGGGTGATTGGAAGCAAGTCTCTGCTCGAGGAAT 194
QY 181 GCGGAGCATCGGGGAGGAGCTTGAGAGAGGCTCCGCGAAGCGACGACGCGGAGTCT 240
DB 181 GCGGAGCATCGGGGAGGAGCTTGAGAGAGGCTCCGCGAAGCGACGACGCGGAGTCT 240
QY 195 GCGGAGCATCGGGGAGGAGCTTGAGAGAGGCTCCGCGAAGCGACGACGCGGAGTCT 254
DB 195 GCGGAGCATCGGGGAGGAGCTTGAGAGAGGCTCCGCGAAGCGACGACGCGGAGTCT 254
QY 241 TCCTTGAAGAGAGGCTGTAAACCCGCGAGCAAGCCAGTCGACGACCCCGAGAGAG 300
DB 241 TCCTTGAAGAGAGGCTGTAAACCCGCGAGCAAGCCAGTCGACGACCCCGAGAGAG 300
QY 255 TCCTTGAAGAGAGGCTGTAAACCCGCGAGCAAGCCAGTCGACGACCCCGAGAGAG 314
DB 255 TCCTTGAAGAGAGGCTGTAAACCCGCGAGCAAGCCAGTCGACGACCCCGAGAGAG 314
QY 301 GTTGCTTCGAGGTCCTGATGACCATATATCAACAGCAGGCTCGACATCTTTGTTAT 360
DB 301 GTTGCTTCGAGGTCCTGATGACCATATATCAACAGCAGGCTCGACATCTTTGTTAT 360
QY 315 GTTGCTTCGAGGTCCTGATGACCATATATCAACAGCAGGCTCGACATCTTTGTTAT 374
DB 315 GTTGCTTCGAGGTCCTGATGACCATATATCAACAGCAGGCTCGACATCTTTGTTAT 374
QY 361 CTGCTGCGGCTTACGCAACCCGATGACGACTGCTGGCGGTGCGACCCCTGATTGCGAT 420
DB 361 CTGCTGCGGCTTACGCAACCCGATGACGACTGCTGGCGGTGCGACCCCTGATTGCGAT 420

Oy GTCAACACAAAAAGCTGCTGACTGGGGCAATTGGCTTTGGACGCAACGNATNANGTGC 480
 Db GTCAACACAAAAAGCTGCTGACTGGGGCAATTGGCTTTGGACGCAACGNATNANGTGC 494
 Oy CGCAGCGGGGAAATTGGTCTGTTGTGACAGACTCGGGGGACNATGATTCGCCGTGATCCTC 540
 Db CGCAGCGGGG -AGTTGTACGTTGTGTGACAGACTCGGGGGACAGATGAT -CCGCTGAATCCTC 552
 Oy GCCCGGGGAACCTTANATACCCCGCTCNTCCAAANGAAGTTGCCCCCTCTGGAGTCCCTTT 600
 Db GCCCGGGGAACCTTAGATACCGCGCTCAATCC - - -AGGACGTGCCCTCTGGATCACTTT 608
 Oy AAACNCNAAATGGAATCTCNCNTCNANGAAGAAGTCTTTATGAACACTTTAANACAT 660
 Db AAACACGACATGAGATACGCTC -AAGGAAGAAGTCAATTATGAACAACTTTAAGAGCAT 667
 Oy CGATGGACNCGTGTCTGTCCACATTTGGCCAAATGGGCGCTGCNCTACACANCAATTTCN 720
 Db CGATGGACGCGGTGTCAACGTCACATTTGCCAAATGGGCGCTGCATCACACATTC -AGTACA 726
 Oy TCCCAACATCTTTCTTCNTNNGCCTCNC - -TCCCAATGCACCCNCGGGAATTCCTN 778
 Db TCACCAACGTCATCATCCACGCGCTCCACATCCACAGACTGCAGAGCCACCGGGAATGCCA 786
 Oy GTCCCCNCTCCCTTCTCTCATGATNG 806
 Db TGTGTCCGAGCTCTCTCTCATGATNG 814

RESULT 3				
AB3011	AB3011	748 bp	DNA	linear
LOCUS	Sequence 18 from Patent WO9853085.			
DEFINITION				
ACCESSION	AB3011			
VERSION	AB3011.1	GI:6732491		

-ORGANISM
 unidentified.
 unclassified.
 REFERENCE
 1 (bases 1 to 748)
 AUTHORS
 Seymour G.B. and Bird C.R.
 TITLE
 GENETIC COMBOST-OF PUUT RIPPENING
 :JOURNAL
 Patent: WO 983085-A 18 26-NOV-1998;
 SETMOOR GRAHAM BARON (GB); ZENECA LTD (GB)
 FEATURES
 Location/Qualifiers
 1..748

BASE COUNT	154 a	211 c	206 g	163 t	14 others
ORIGIN					
Query Match	73.4%	Score 591.8:	DB 6:	Length 748:	
Best Local Similarity	91.7%	Pred. No. 2.5e14:			
Matches 664: Conservative	0:	Mismatches 52:	Indels 8:	Gaps 4:	

[illegible]

OY	24	TCCTTGGAAAGAGAGGGCTGTAACCCGGGGACACAGAACCGCAGTGCAGACCCCCAGAG	300
Db	256	TCCTTGGAAAGAGAGGGCTGTAAACCAGGGCAGACAGACCCGAGTGCAGACCCCCAGAG	315
OY	301	GTTGCTTTCGACGGTCTGTGATGACATAATACACAGACAGCGCTCGAGATCTCTTGTTAT	360
Db	316	GTTGCTTTCGACGGTCTGTGACGACCATTAATACACAGACAGCGCTCGAGATCTCTTGTTAT	375
OY	361	CTGTGCGAGGGTTTAGGCAACCCGATGAGACACGTGGGGGTGGGACCCGATGGCAT	420
Db	376	CTGTGCGAGGGTTTAGGCAACCCGATGAGACACGTGGGGGTGGGACCCGATGGCAT	435
OY	421	GTCACAGAAAAAAGCTCGCTGACTGCGGCACTTGGCTTGGACGCAACGNAATANGTGC	480
Db	436	GTCACAGAAAAAAGCTCGCTGACTGCGGCACTTGGCTTGGACGCAACGCAATAGTGGC	495
OY	481	CGGAGCGGGGGAATTTGTTGTTGGACAGACTCGGGGGACNAATGATCCCGGTGATCTTC	540
Db	496	CGGAGCGGGGGAATTTGTTGTTGGACAGACTCGGGGGACNAATGATCCCGGTGATCTTC	555
OY	541	GCCCGGGAGACCTAANATACCCCGCTCNCACANAAGTTGCCCCCTCGGAGTCCCTTT	600
Db	556	CCCGGGAGACCTAANATACCGCTCATCANGACTG----CCCTCTGGATCNCCTTT	610
OY	601	AAACNCNAATNGGAATCTCNCNCNANAGGAAGAAGTCTTTATGAACACCTTAAACAAAT	660
Db	611	AAACACCAACNTGGANATACCTCTCA-GGAAGAACTCTTATGAACACCTTAAACAAAT	669
OY	661	CGATGACACNCNGTCTCTCTGTCACATTTGCCAATGGGCGCTGCNTCACANCAATTTCN	720
Db	670	CGATGACAC-CCGTGTTCACGTCACACTTGGCCAAATGGC-CTGCNTACACATTCACANTCNT	727
OY	721	TTCC 724	
Db	728	CACC 731	

RESULT 4				
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LOCUS	AB33004	745 bp	DNA	Linear
DEFINITION	Sequence '11 from Patent WO9853085.			
ACCESSION	AB33004			
VERSION	AB33004.1	GI:6732464		
KEYWORDS	unidentified.			
SOURCE	unidentified			
ORGANISM	unclassified.			
REFERENCE	1 (bases 1 to 745)			
AUTHORS	Seymour, G.B. and Bird, C.R.			
TITLE	GENETIC CONTROL OF FRUIT RIPENING			
JOURNAL	Patent: WO 9853085-A 11 26-NOV-1998;			
FEATURES	SEYMOUR GRAHAM BARRON (GB); ZENECA LTD (GB)			
	Location/Qualifiers			

	source	1. .745 /organism="unidentified" /db_xref="taxon:32644" /clone="U-52"
BASE COUNT	153 a	204 c 203 g 163 t 22 others
ORIGIN	-	
Query Match	73.3%; Score 591.2; DB 6; Length 745;	
Best Local Similarity	90.5%; Pred. No. 3.7e-144;	
Matches 673; Conservative	0; Mismatches 61; Indels 10; Gaps 5;	
Oy	1 TGTTCCTCCATCATCATCTTTTGGCTGTGGAAACGTGAGAGTGAGACGAGGCG 60	
Db	7 TGTTCCTCCATCATCATCTTTTGGCTGTGGAAACGTGAGAGTGAGACGAGGCG 66	
Oy	61 GCATGACGGGGGTTAAGTGAATCCCTCTGCTCTTCCTCTCGGGCTTCCTG 120	
Db	67 GCATGACGGGGGTTAAGTGAATCCCTCTGCTCTTCCTCTCGGGCTTCCTG 126	
Oy	121 CTGGTTTTGAACGGAGGTCGGGGGTGAGTTGGAACGAGAGGTCCTCTGCTCGAGGAT 180	

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Db      127 CTGTTTGAACGAGAGTGGGGGTGATTGGAAGCAGAGAGTCTGCTCGAGAAAT 186
Oy      181 GGGGAGCATCGCGGAGAGCTTGAGAGAGGCTCCGGAACGCGACAGCGCGATGCT 240
Db      187 GGGGAGCATCGCGGAGAGCTTGAGAGAGGCTCCGGAAGCGGACCGAGCGATGCT 246
Oy      241 TCCTTGAAGAGAGGCTGTAAACCGGGCAGACAGACCGGAGTGCAGAGCCCGAGAG 300
Db      247 TCCTTGAAGAGAGGCTGTAAACCGGGCAGACAGACCGGAGTGCAGAGCCCGAGAG 306
Oy      301 GTTGCTTCGACGGTCTGATGATGACATTAATCAACAGCAGGCTCGCAATCTTTGTTAT 360
Db      307 GTTGCTTCGACGGTCTGATGATGACATTAATCAACAGCAGGCTCGCAATCTTTGTTAT 366
Oy      361 CTGCTGTGAGGCTTGAAGCAGACCGGATGACAGCTGCGGGGCTCGAGCCGATTTGGCAT 420
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Oy      480 CCGGAGAGGGAATTTGTTGTTGTGACAGACTCCGGGAGCMATGATCCCGTGAATCT 539
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Oy      540 CCGGAGAGGGAATTTGTTGTTGTGACAGACTCCCGTGAATGTTGCGGCTGCGGATCCCT 599
Db      545 CCGGAGAGGGAATTTGTTGTTGTGACAGACTCCCGTGAATGTTGCGGCTGCGGATCCCT 600
Oy      600 TAAACNCNMAANTGGAATCTCNCNTCANGAAGAACTNTTANGAACAGC--TTTANA 656
Db      601 TAAACNCNMAANTGGAATCTCNCNTCANGAAGAACTNTTANGAACAGC--TTTANA 660
Oy      657 CMTGATGACACNCGTCTGCTGTCACATGCGCATGCGGCTCGTCAACCAAT 716
Db      661 ACATGCGAGTGAACCGTCTGTCNCNTCCACATGCGCAATGCGGCTGCTTCAACCAAT 720
Oy      717 TTCNTCCCAACNTCTCTCCNT 740
Db      721 TACATCACAACGTCATCTCCAT 744

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RESULT 5
 A83001
 LOCUS A83001
 DEFINITION Sequence 8 from Patent W09853085.
 ACCESSION A83001.1 GI:6732481
 VERSION A83001.1 GI:6732481
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 793)
 AUTHORS Seymour, G.B. and Bird, C.R.
 TITLE GENETIC CONTROL OF FRUIT RIPENING
 JOURNAL Patent: WO 9853085-A 8 26-NOV-1998;
 SEYMOUR GRAHAM BARON (GB); ZENECA LTD (GB)
 FEATURES
 Source
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 BASE COUNT 170 a 222 c 215 g 171 t 15 others
 ORIGIN

Query Match 73.1%; Score 588.8; DB 6; Length 793;
 Best Local Similarity 88.7%; Pred. No. 1.6e-143;
 Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;
 Oy 1 TGTTCCTCTCTGATCACAATCTTTTGTCTGTGGAACGCTGAGGTGACGAGGCG 60
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Db      8 TGTTCCTCTCTGATCACAATCTTTTGTCTGTGGAACGCTGAGAGGTGACGAGGCG 67
Oy      61 GCATGACGGGCGGTTTAAGATGATTCCTCTGCTTCTTCTTCTGCGCTCTG 120
Db      68 GCATGACGGGCGGTTTAAGATGATTCCTCTGCTTCTTCTTCTTATGCGCTTCTG 127
Oy      121 CTGTTTTGAACGAGAGTGGGGGTGATTGGAAGCAGAGAGTCTTGCTCGAGAAAT 180
Db      128 CTGTTTTGAACGAGAGTGGGGGTGATTGGAAGCAGAGAGTCTTGCTCGAGAAAT 187
Oy      181 GGGGAGCATCGCGGAGAGCTTGAGAGAGGCTCCGGAACGCGACAGCGCGATGCT 240
Db      188 GGGGAGCATCGCGGAGAGCTTGAGAGAGGCTCCGGAACGCGACAGCGCGATGCT 247
Oy      241 TCCTTGAAGAGAGGCTGTAAACCGGGCAGACAGACCGGAGTGCAGAGCCCGAGAG 300
Db      248 TCCTTGAAGAGAGGCTGTAAACCGGGCAGACAGACCGGAGTGCAGAGCCCGAGAG 307
Oy      301 GTTGCTTCGACGGTCTGATGATGACATTAATCAACAGCAGGCTCGCAATCTTTGTTAT 360
Db      308 GTTGCTTCGACGGTCTGATGATGACATTAATCAACAGCAGGCTCGCAATCTTTGTTAT 367
Oy      361 CTGCTGTGAGGCTTGAAGCAGACCGGATGACAGCTGCGGGGCTCGAGCCGATTTGGCAT 420
Db      368 CTGCTGTGAGGCTTGAAGCAGACCGGATGACAGCTGCGGGGCTCGAGCCGATTTGGCAT 427
Oy      421 GTCACACAG-AAAAAGCTCGCTGACTCGGCAATTGGCTTGGACGCAACGCMATANGTG 479
Db      428 GTCACACAGAAAAAGCTCGCTGACTCGGCAATTGGCTTGGACGCAACGCMATANGTG 487
Oy      480 CCGGAGAGGGAATTTGTTGTTGTGACAGACTCCGGGAGCMATGATCCCGTGAATCT 539
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Oy      540 CCGGAGAGGGAATTTGTTGTTGTGACAGACTCCCGTGAATGTTGCGGCTGCGGATCCCT 599
Db      547 CCGGAGAGGGAATTTGTTGTTGTGACAGACTCCCGTGAATGTTGCGGCTGCGGATCCCT 602
Oy      600 TAAACNCNMAANTGGAATCTCNCNTCANGAAGAACTNTTANGAACAGC--TTTANA 659
Db      603 TAAACNCNMAANTGGAATCTCNCNTCANGAAGAACTNTTANGAACAGC--TTTANA 660
Oy      660 TCGATGACACNCGTCTGCTGTCACATGCGCATGCGGCTCGTCAACCAATTTTC 719
Db      661 TCGATGACACCGG--TGTACAGTCCACATGCGCAATGCGGCTGCTTCAACCAATCA 717
Oy      720 NTCCCAACACNTCTCTCNCNTCANGAAGAACTNTTANGAACAGC--TTTANA 777
Db      718 ATCACCAACNTCAATGCGCTTCCACNTCCACAAATGCNACCCAGGAATNGCT 777
Oy      778 NGTCCCGCTCCCT 792
Db      778 TGTTCCTCTCTGATCACAATCTTTTGTCTGTGGAACGCTGAGGTGACGAGGCG 792

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RESULT 6
 MA29965
 LOCUS MA29965
 DEFINITION Musa acuminata mRNA for putative pectate lyase (type I) (clone pBAN E022).
 ACCESSION MA29965
 VERSION 29965
 KEYWORDS
 SOURCE Musa acuminata.
 ORGANISM Musa acuminata.
 REFERENCE 1 (bases 1 to 793)
 AUTHORS Druy, R., Hortonsteiner, S., Donnison, I., Bird, C.R. and Seymour, G.B.
 TITLE Chlorophyll catabolism and gene expression in the peel of ripening banana fruits
 JOURNAL Physiol. Plantarum 107, 32-38 (1999)

REFERENCE 2 (bases 1 to 793)
 AUTHORS Medina-Suarez, R.
 TITLE Direct Submission
 JOURNAL Submitted (17-OCT-1997) R. Medina-Suarez, Horticulture Research International, Wellesbourne, Warwick, CV35 9EF, UNITED KINGDOM
 FEATURES Location/Qualifiers
 source 1..793
 /organism="Musa acuminata"
 /cultivar="Grand Nain"
 /db_xref="taxon:4641"
 /clone="PBAN EU22"
 /cell_line="X10LR"
 /tissue_type="fruit peel"
 /note="Musa AAA group"
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 /product="pectate lyase (type I)"
 /note="putative"
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 BASE COUNT 170 a 222 c 215 g 171 t 15 others
 ORIGIN
 Query Match 73.1%; Score 588.8; DB 8; Length 793;
 Best Local Similarity 88.7%; Pred. No. 1.6e-143;
 Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;
 QY 1 TGTTCCTCCTTCGATCAGATCTTTTGGCTGGGAAAGCTGAGAGTGAAGAGGCG 60
 DB 8 TGTTCCTCCTTCGATCAGATCTTTTGGCTGGGAAAGCTGAGAGTGAAGAGGCG 67
 QY 61 GCAATGACGGGGGTTTAAAGATGATTCCTCTGCTCTTCTTCTTGGGCTTCG 120
 DB 68 GCAATGACGGGGGTTTAAAGATGATTCCTCTGCTCTTCTTCTTGGGCTTCG 127
 QY 121 CTGGTTTAAAGAGAGTGGGGGGTGGATTTGAAGAGAGAGTCCCTGCTCGAGGAT 180
 DB 128 CTGGTTTAAAGAGAGTGGGGGGTGGATTTGAAGAGAGAGTCCCTGCTCGAGGAT 187
 QY 181 GCGGAGCATCGCGGAGAGCTTGAAGAGGCTCCGCAACGCGACGCGCGGATGCT 240
 DB 188 GCGGAGCATCGCGGAGAGCTTGAAGAGGCTCCGCAACGCGACGCGCGGATGCT 247
 QY 241 TCCCTTGAAGAGAGGCTTAAACCGGCGAGCAGAAAGCCGAGTCGACGCCCGAGAG 300
 DB 248 TCCCTTGAAGAGAGGCTTAAACCGGCGAGCAGAAAGCCGAGTCGATGACCCGAGAG 307
 QY 301 GTTGTTCGACGGTCTCTGATGACATTAATCAACAGACGCTCGCATCTTGGTTAT 360
 DB 308 GTTGTTCGACGGTCTCTGATGACATTAATCAACAGACGCTCGCATCTTGGTTAT 367
 QY 361 CTGTGTGGGTTGAGGCAACCGGATCGACGACTGCTGGGGTGGGACCTGATGGCAT 420
 DB 368 CTGTGTGGGTTGAGGCAACCGGATCGACGACTGCTGGGGTGGGACCTGATGGCAT 427
 QY 421 GTCAACAG-AAAAAGCTGCTGACTGCGGCAATTGGCTTTGAGCGCAACGCAATANGTG 479
 DB 428 GTCAACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGAGCGCAACGCAATANGTG 487
 QY 480 CCGCGACGGGGAATTTGTTGTTGTGACAGACTCCGGGAGCAATATATATATATATATAT 539
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 QY 540 CCGCGGGAACACTTANATACCCGCTCCTCCCAANGAAGTTGCCCTCTGGGATCCCTT 599
 DB 547 GCCCGGGGAACACTTANATACCCGCTCCTCC-ANGACGTGCCCTCTGGATCACTT 602
 QY 600 TAAACNCAANTGAAATCTCNCCTNANGAAGAACTGTTATGAAACACTTTTANANCA 659
 DB 603 TAAACGACATGAAATCACTCC-AGGAAGAACTGTTATGAAACNCTTTANANCA 660
 QY 660 TCGATGACACNCTGTCTGTCACATTTGCAATGCGGCTGCTGACCAACCAATTCCT 719
 DB 661 TCGATGACACCG--TGTCAAGTCCACATTTGCAATGCGGCTGCTGACCAACCA-TTA 717
 QY 720 TTCGCCAACNTCTTCTCCTGCTGCTCCT--CCCAATGCAACCCGCGGAATTCCT 777

DB 718 ATCACCACNTATCTTCATGCGCTCCACACNTCCACAAATGCAACCCACCGAATNCT 777
 QY 778 NGTCCCTCCCTCCCT 792
 DB 778 TGTCTCCACTCTCT 792
 RESULT 7
 A83014 727 bp DNA linear PAT 21-JAN-2000
 LOCUS Sequence 21 from Patent WO9853085.
 DEFINITION A83014
 ACCESSION A83014
 VERSION A83014.1 GI:6732494
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 727)
 AUTHORS Seymour, G.B. and Bird, C.R.
 TITLE GENETIC CONTROL OF FRUIT RIPENING
 JOURNAL Patent: WO 9853085-A 21 26-NOV-1998;
 SEYMOUR GRAHAM BARRON (GB); ZENECA LTD (GB)
 FEATURES Location/Qualifiers
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 /organism="unidentified"
 /db_xref="taxon:32644"
 /clone="U-139"
 BASE COUNT 144 a 199 c 202 g 157 t 25 others
 ORIGIN
 Query Match 71.0%; Score 572.2; DB 6; Length 727;
 Best Local Similarity 90.9%; Pred. No. 3.5e-139;
 Matches 653; Conservative 0; Mismatches 57; Indels 8; Gaps 5;
 QY 1 TGTTCCTCCTTCGATCAGATCTTTTGGCTGGGAAAGCTGAGAGTGAAGAGGCG 60
 DB 16 TGTTCCTCCTTCGATCAGATCTTTTGGCTGGGAAAGCTGAGAGTGAAGAGGCG 75
 QY 61 GCAATGACGGGGGTTTAAAGATGATTCCTCTGCTCTTCTTCTTGGGCTTCG 120
 DB 76 GCAATGACGGGGGTTTAAAGATGATTCCTCTGCTCTTCTTCTTGGGCTTCG 135
 QY 121 CTGGTTTAAAGAGAGTGGGGGGTGGATTTGAAGAGAGAGTCCCTGCTCGAGGAT 180
 DB 136 CTGGTTTAAAGAGAGTGGGGGGTGGATTTGAAGAGAGAGTCCCTGCTCGAGGAT 195
 QY 181 GCGGAGCATCGCGGAGAGCTTGAAGAGGCTCCGCAACGCGACGCGCGGATGCT 240
 DB 196 GCGGAGCATCGCGGAGAGCTTGAAGAGGCTCCGCAACGCGACGCGCGGATGCT 255
 QY 241 TCCCTTGAAGAGAGGCTTAAACCGGCGAGCAGAAAGCCGAGTCGACGACCCGAGAG 300
 DB 256 TCCCTTGAAGAGAGGCTTAAACCGGCGAGCAGAAAGCCGAGTCGACGACCCGAGAG 315
 QY 301 GTTGTTCGACGGTCTCTGATGACATTAATCAACAGACGCTCGCATCTTGGTTAT 360
 DB 316 GTTGTTCGACGGTCTCTGATGACATTAATCAACAGACGCTCGCATCTTGGTTAT 375
 QY 361 CTGTGTGGGTTGAGGCAACCGGATCGACGACTGCTGGGGTGGGACCTGATGGCAT 419
 DB 376 CTGTGTGGGTTGAGGCAACCGGATCGACGACTGCTGGGGTGGGACCTGATGGCAT 435
 QY 420 TGTCAACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGAGCGCAACGCAATANGTG 479
 DB 436 TGTCAACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGAGCGCAACGCAATANGTG 495
 QY 480 CCGCGACGGGGAATTTGTTGTTGTGACAGACTCCGGGAGCAATATATATATATATATAT 539
 DB 496 CCGCGACGGGGA-ATTGTCNCTTGTGACAGACTCCGGGAGCAATATATATATATATAT 554
 QY 540 CCGCGGGAACACTTANATACCCGCTCCTCCCAANGAAGTTGCCCTCTGGGATCCCTT 599
 DB 540 CCGCGGGAACACTTANATACCCGCTCCTCC-ANGACGTGCCCTCTGGATCACTT 602

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Db      555  CCCCCGGAACNCTTANATACGCCGTCATCC----ANGACTNCCCCTCTGAGTACCTTT 610
Qy      600  TAAACNMAANTGGAATCTCNCNANGAAGAAGACTNTATGACAGCTTTTAAACNA 659
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Db      611  TAAACNCACTATGANNATCCGCCCA-GGAAGAATCATATATGACAGCTTTTAAACNA 669
Qy      660  TCGATGACNCTGCTCCTGTCACATTTGCCAATGGCGCTGCTACCAACCAAT 717
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      670  TCGATGAC-CCGTCGTCAGCTCNCNTTGGCAATGGGCGCTGCTCNCNTCNCNTT 726

RESULT 8
A70155  A70155 727 bp DNA Linear PAT 07-MAY-1999
DEFINITION Sequence 16 from Patent WO9811228.
ACCESSION A70155
VERSION A70155.1 GI:4774570
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 727)
AUTHORS Seymour,G.B., Bird,C.R. and Medina-Suarez,R.D.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9811228-A 16 19-MAR-1998;
FEATURES
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        /clone="U-089"

BASE COUNT 145 a 205 c 196 g 159 t 22 others
ORIGIN
Query Match 67.5% Score 543.8 DB 6; Length 727;
Best Local Similarity 86.6% Pred. No. 9.8e-12;
Matches 62; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

Qy      2  GTCTCTCTCGATCATCATCTTTTCTGCTGGGAACGTGAGAGTGAGACGAGCGG 61
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Db      8  GTCTCTCTCGATCATCATCTTTTCTGCTGGGAACGTGAGAGTGAGACGAGCGG 67
Qy      62  CAATGACGGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
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Db      68  CAATGACGGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
Qy      122  TGGTTTGAACGAGGAGCGGGGGTGATGGAAGCGAGGCTCTGCGCGAGGATG 181
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      128  TGGTTTGAACGAGGAGCGGGGGTGATGGAAGCGAGGCTCTGCGCGAGGATG 187
Qy      182  GCGGAGCATGCGGAGGAGGCTTGAGAGAGGCTCCGCGAAGCGGACGAGCGGATCTT 241
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Db      188  GCGGAGCATGCGGAGGAGGCTTGAGAGAGGCTCCGCGAAGCGGACGAGCGGATCTT 247
Qy      242  CTTTGAAGAGAGGCGCTTAACCGGCGACAGAACCGCAAGTCGACAGACCCGAGAGG 301
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Db      248  CTTTGAAGAGAGGCGCTTAACCGGCGACAGAACCGCAAGTCGACAGACCCGAGAGG 307
Qy      302  TTCTTTCGACGCTCTGATACCATATCAACAGACGAGGTCGAGATCTTTGGTATC 361
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Db      308  TTCTTTCGACGCTCTGATACCATATCAACAGACGAGGTCGAGATCTTTGGTATC 367
Qy      362  TGTGTCGCGGTTAGGCAACCGATGACAGCTGTGCGGTGCGAGCCCTGATTTGGCATG 421
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Db      368  TGTGTCGCGGTTAGGCAACCGATGACAGCTGTGCGGTGCGAGCCCGATTTGGCATG 427
Qy      422  TCAACGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGG-ACGCAACGCAATANGTGC 480
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Db      428  TCAACGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGG-ACGCAACGCAATANGTGC 487
Qy      481  CCGGAGCGGGAATTTGTTGTTGTCGACAGACTCCGGGACNATGATCCCGTGAATCTC 540
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Db      488  CCGGAGCGGGAATTTGTTGTTGTCGACAGACTCCGGGACNATGAT-CCCGTGAATCTC 546

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Qy      541  GCCCGGAACACTTANATACCCGCTCNCNANGAAGTTGCCCTCTGGAGTCCCTTT 600
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Db      547  CCCCCGAACACTTANATATTCCTCCGTCATCCAG---ANCNCCCCTCTGATCTMCCTTT 603
Qy      601  AACNMAANTGGAATCTCNCNANGAAGAAGCTNTATGACAGCTTTTAAACNAT 660
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Db      604  AAGACGACATTTGGA-ATCNCNCCCNGAAGAACTCCTTTTAAACGCTTTNNAACATC 662
Qy      661  CGATGACNCTGCTCCTGTCACATTTGCCAATGGGCGCTGCTACCAACCAATTCN 720
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Db      663  NATGACNCTGCTCCTCCTGTCACATTTGCCAATGGGCGCTGCTCNCNCAACNATTTAA 722
Qy      721  TCCCC 725
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Db      723  TCNCC 727

RESULT 9
A70157  A70157 724 bp DNA Linear PAT 07-MAY-1999
DEFINITION Sequence 18 from Patent WO9811228.
ACCESSION A70157
VERSION A70157.1 GI:4774572
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 724)
AUTHORS Seymour,G.B., Bird,C.R. and Medina-Suarez,R.D.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9811228-A 18 19-MAR-1998;
FEATURES
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BASE COUNT 143 a 201 c 197 g 155 t 28 others
ORIGIN
Query Match 66.5% Score 536 DB 6; Length 724;
Best Local Similarity 89.7% Pred. No. 1.1e-12;
Matches 61; Conservative 0; Mismatches 62; Indels 9; Gaps 5;

Qy      6  TCTCTCGATCATCATCTTTTCTGCTGGGAACGTGAGAGTGAGACGAGGCGCAAT 65
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Db      9  TCTCTCGATCATCATCTTTTCTGCTGGGAACGTGAGAGTGAGACGAGGCGCAAT 68
Qy      66  GAGCGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125
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Db      69  GAGCGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 128
Qy      126  TTTGAACGAGGCTGCGGGGGTGATTTGAACGAGAGGTCCTCTGCTGAGGAATGGCG 185
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      129  TTTGAACGAGGCTGCGGGGGTGATTTGAACGAGAGGTCCTCTGCTGAGGAATGGCG 188
Qy      186  AGCATGCGGAGGAGCTTTGAGAGAGGCTCCGCGAAGCGGACGAGCGGATCTTCTT 245
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Db      189  AGCATGCGGAGGAGCTTTGAGAGAGGCTCCGCGAAGCGGACGAGCGGATCTTCTT 248
Qy      246  GGAAGAGGAGGCTGTAACCCGCGAGAGAGCGGAGTCGACGACCCGAGAGGTTGC 305
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Db      249  GGAAGAGGAGGCTGTAACCCGCGAGAGAGCGGAGTCGACGACCCGAGAGGTTGC 308
Qy      306  TTTGAGCGTCTCTGATACCATATCAACAGACAGGCTCGAGATCTTTGTTATCTGTC 365
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Db      309  TTTGAGCGTCTCTGATACCATATCAACAGACAGGCTCGAANATCTTTGTTATCTGTC 368
Qy      366  GTGCGGTTAGGCAACCCGATGACAGCTGTGCGGTGCGAGCCGATTTGGATGCA 425
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Db      369  GTGCGGTTAGGCAACCCGATGACAGCTGTGCGGTGCGAGCCGATTTGGATGCA 428

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QY 426 CAGAAAAAGCTGCTGACTGGGCAATGGCTTTGGACGCAACGCNATANGTGCCGCGA 485
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 DB 429 CAGAAAAAGCTGCTGACTGGGCAATGGCTTTGGACGCAACGCNATANGTGCCGCGA 488
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 QY 486 CCGGGAATTTGCTGTTGGACAGACTCCGGGACNATGATCCCGTGATCTCTGCGCG 545
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 DB 489 CCGGG-ANTGTGNCCTTGACAGACTCCGGGACGATGATCCCGTGATCTCTGCGCG 547
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 QY 546 GGAACACTTANATACCCGCTCCCAANGAGTTGGCCCGCTCGGGATCCCTTTAAACN 605
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 DB 548 GGAACACTTANAT-ACCCTCCNCCNCAANTTTCCCTCT--GGATCCCTTTAAAC 603
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 QY 606 CNAANTGAAATCTCNCNANGAAGAACTCNTTATGAAGAC--TTTAAACNATGA 663
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 DB 604 C--ACNTGGAANTCCCGCCNCAAGAACTCCTTATGAAGCTTTTAAACATCGAT 661
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 QY 664 TGGACNCGTCTGCTGCTCCACATGGC 691
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 DB 662 NGACCCNGTTCCACTTCCNCAATNGC 689
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RESULT 10

A83000 704 bp DNA linear PAT 21-JAN-2000
 LOCUS A83000
 DEFINITION Sequence 7 from Patent WO9853085.
 ACCESSION A83000
 VERSION A83000.1 GI:6732480
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified.
 unclassified.
 unclassified.

REFERENCE 1 (bases 1 to 704)
 AUTHORS Seymour, G. B. and Bird, C. R.
 TITLE GENETIC CONTROL OF FRUIT RIPENING
 JOURNAL Patent: WO 9853085-A 7 26-NOV-1998;
 SEYMOUR GRAHAM BARON (GB); ZENECA LTD (GB)
 FEATURES
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BASE COUNT 146 a 190 c 191 g 149 t 28 others
 ORIGIN

Query Match 63.4%; Score 510.8; DB 6; Length 704;
 Best Local Similarity 86.8%; Pred. No. 4.4e-123;
 Matches 603; Conservative 0; Mismatches 86; Indels 6; Gaps 5;

QY 10 CTTGCATCATCTTTTGTCTGTGGAAACGTGAGAGTGAGACGAGGCGCAATGACG 69
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 DB 5 CTTGCATCATCTTTTGTCTGTGGAAACGTGAGAGTGAGACGAGGCGCAATGACG 64
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 QY 70 GCGGTTTAAAGATGATTCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 129
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 DB 65 GCGGTTTAAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 124
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 QY 130 AACGAGTGGGGGCTGATTTGAGAGAGCTCCGGAACGAGAGGCTCTGCTCGAGAAATGGCGAGCA 189
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 DB 125 AACGAGTGGGGGCTGATTTGAGAGAGCTCCGGAACGAGAGGCTCTGCTCGAGAAATGGCGAGCA 184
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 QY 180 TCGCAGAGAGCTTGAAGAGAGCTCCGGAACGAGAGGCTCTGCTCGAGAAATGGCGAGCA 249
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 DB 185 TCGCAGAGAGCTTGAAGAGAGCTCCGGAACGAGAGGCTCTGCTCGAGAAATGGCGAGCA 244
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 QY 250 GAGAGGCTGTAACCGGCGAGAGAGCGGAGTGCAGACGCCGAGAGAGTTGCTTCG 309
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 DB 245 GACAGGCTGTAAACGAGAGAGAGCGGAGTGCAGACGCCGAGAGAGTTGCTTCG 304
 |||
 QY 310 ACGGCTGATGACCATATATCAACAGACGAGGCTGCAATCTCTGTTATCTGCTGC 369
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 DB 305 ACGGCTGATGACCATATATCAACAGAGGCTGCAAAATCTCTGTTATCTGCTGC 364
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 QY 370 GGTTCAGGCAACCCGATCGAGACTGCTGCGGTCGACCCCTGATTTGCATGCAACAG- 428
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DB 365 GGTTCAGGCAACCCGATCGACNACTGCTGGCGGTGGACCCGATTTGGCATGCAACAGA 424
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 QY 429 AAAAAAGCTGCTGACTGGGCAATGGCTTTGGACGCAACGCNATANGTGCCGCGAG 488
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 DB 425 AAAAAAGCTGCTGACTGGGCAATGGCTTTGGACGCAACGCNATANGTGCCGCGAG 484
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 DB 485 GG-ANTGTGNCCTTGACAGACTCCGGGACGATGAT-CCCGTGATCTCTGCGCGGA 542
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 QY 549 ACACCTTANATAC-CCGCTCCNCCCAANGAAGTTGCCCGCTCTGGATCCCGTTAAACN 607
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 QY 608 AANTGGAATCTCNCNANGAAGAACTCNTTATGAACGCTTTAANCAATCGATGA 667
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 DB 601 ACNTGGAANTCTCCGCTCCNANGANGAACCTTATGAACNTCTTTAANCAATCA 660
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 QY 668 CMCNGTCTGCTGCTGCTCCATTCGCAATGGCGGCTG 702
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 DB 661 ATGACNCCNGTGTCCACTCCACNTTTCANTG 695
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RESULT 11

A83012 706 bp DNA linear PAT 21-JAN-2000
 LOCUS A83012
 DEFINITION Sequence 19 from Patent WO9853085.
 ACCESSION A83012
 VERSION A83012.1 GI:6732492
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified.
 unclassified.
 unclassified.

REFERENCE 1 (bases 1 to 706)
 AUTHORS Seymour, G. B. and Bird, C. R.
 TITLE GENETIC CONTROL OF FRUIT RIPENING
 JOURNAL Patent: WO 9853085-A 19 26-NOV-1998;
 SEYMOUR GRAHAM BARON (GB); ZENECA LTD (GB)
 FEATURES
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 /db_xref="taxon:32644"
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BASE COUNT 144 a 192 c 195 g 153 t 22 others
 ORIGIN

Query Match 61.6%; Score 496.8; DB 6; Length 706;
 Best Local Similarity 90.6%; Pred. No. 2.1e-119;
 Matches 639; Conservative 0; Mismatches 52; Indels 14; Gaps 10;

QY 2 GTTCTCTCTGATCATCTTTTGTCTGTGGAAACGTGAGAGTGAGACGAGGCGG 61
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 DB 7 GTTCTCTCTGATCATCTTTTGTCTGTGGAAACGTGAGAGTGAGACGAGGCGG 66
 |||
 QY 62 CAATAGCGGCGGCTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
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 DB 67 CAATAGCGGCGGCTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 126
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 QY 122 TGGTTTGAACGAGAGTGGGGGCTGATTTGAAGAGAGGCTCTGCTCGAAGAAATG 181
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 DB 127 TGGTTTGAACGAGAGTGGGGGCTGATTTGAAGAGAGGCTCTGCTCGAAGAAATG 186
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 QY 182 GCGAGCATCGCGAGAGACTTGAAGAGAGCTCCGGAACGAGAGCGGAGTGTCT 241
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 DB 187 GCGAGCATCGCGAGAGACTTGAAGAGAGCTCCGGAACGAGAGCGGAGTGTCT 246
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 QY 242 CTTGGAAGAGAGGCTGTAACCGGCGGAGAGCGGAGTGCAGACGCCGAGAGG 301
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 DB 247 CTTGGAAGAGAGGCTGTAACCGGCGGAGAGCGGAGTGCAGACGCCGAGAGG 306
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 QY 302 TTGCTTCAGGCTCTGATGACCATATCAACAGACGAGTGCAGATCTTGGTTATC 361
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identified by repeatmasker (Arian Smil,
http://ftp.genome.washington.edu/RM/RepeatMasker.html).

FEATURES
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location/Qualifiers
1. 90142
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join(<1019. 1121,1318. 1389,1497. 1562,1659. 1715. 1809. 1876,1964. 2045,2248. 2303,2386. 2688,2790. 2876. 3005. 3179,3256. 3377,3477. 3640,3750. 4004,4085. 4206. 4288. 4409,4506. 4654,4751. 4889,5067. >5102)
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Query Match 18.9%; Score 152; DB 8; Length 90142;

Best Local Similarity 63.5%; Pred. No. 5.6e-29;

Matches 277; Conservative 0; Mismatches 152; Indels 7; Gaps 4;

OY 317 TCATGACCATATCAACAGCAGCGGCTCGAGATCTCTGTTATCTGTCGCGGTTCAG 376
DB 53474 TAGAGGACATTGGAACACACAGAGCGAGAAATTAGGTACTTCTCTGCGCCACG 53415
OY 377 GCACCCGATCGACAGACTGCTGCGGTGCGACCTGATGTCATGCAAGAAAAAGC 436
DB 53414 GCACCCGATCGACAGACTGCTGCGGTGCGACCTGATGTCATGCAAGAAAAAGC 53355
OY 437 TCGTACATCGCGCATGCTGTTGACAGCAACGCAATGATGCGCGGAGAAATTG 496
DB 53354 TAGCGGATTCATACGATTTGGCCGACAGCAATCGAGGCGCGAC-GGTGCTTTC 53296
OY 497 TTGCTTGACAGACTCGCGGAGCAATGATCGCGGATCGCGCGGAGAACTTAN 556
DB 53295 TAGCTGTAACGACCGCTGAGACAGCAT-CCCGTAAATCCCATACGCGAAGACTCGG 53237
OY 557 ATACCCCGCTCTCAAGAGATTGCCCTCTGGGATCCCTTTAAACNCNANTGGA 616
DB 53236 TCACGCGGTGATTC---AAGACGAACACACTCTGATCATCTTCAACGCGCATGTGA 53181
OY 617 TCTCNCCTCANGAAGAACTCTTATGAACAGCTTTAANANNCNANTGAGACNCTGTC 676
DB 53180 TAAC-CTTGACAGCAAGAGCTGATCATGACACTTCAAAACCATGATGCTGTGTC 53122
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DB 53121 AATGTTACATGCTAATGAGCTGTCTACGATTCATTAACATTAATTTGTC 53062
OY 737 CCNTGACCTCCNCTCC 752
DB 53061 CATGGATTCATGTC 53046

RESULT 15
LOCUS AB3003 823 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 10 from Patent WO9853085.
ACCESSION AB3003
VERSION AB3003.1 GI:6732483
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 823)
AUTHORS Seymour,G.B. and Bird,C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 10 26-NOV-1998;
SEYMOUR GRAHAM BARON (GB); ZENECA LTD (GB)
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ORIGIN

Query Match 18.7%; Score 151; DB 6; Length 823;
Best Local Similarity 63.7%; Pred. No. 9.9e-29;
Matches 272; Conservative 0; Mismatches 149; Indels 6; Gaps 4;

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OY 387 CGACGACTGCTGGCGTCGACCGCATGATGTCATGCAACAAAAAGCTCGCTGACTG 446

DB 197 CGACGACTGCTGCGGTGCGATCTGACCTGGGCGGACAGCCGCGCTCGCGGACTG 256
OY 447 CGGCAATGCTTTGACGCAACGCNANTANGTGCGCGGCGGAGAAATTTGTTCTGTGA 506
DB 257 CGGCAATGCTTTGACGCAACGCNANTANGTGCGCGGCGGAGAAATTTGTTCTGTGA 315
OY 507 CAGACTCGCGGAGCAATGATCCCGGATTCGCGCGGAGAACTTANATACCCGCTC 566
DB 316 CGGCAATGCTTTGACGCAACGCNANTANGTGCGCGGCGGAGAAATTTGTTCTGTGA 374
OY 567 ATCAAGAGAGGAGCGCGCTGT---GGATCATCTTCAAGCGGAGCATGTGTCATC-CAATTGA 430
DB 375 ATCAAGAGAGGAGCGCGCTGT---GGATCATCTTCAAGCGGAGCATGTGTCATC-CAATTGA 430
OY 627 NGAGAGACTCTTATGAACAGCTTTAANANNCNANTGATGAGACNCTGTCGTCACA 686
DB 431 AAGAGAGCTCATATGAACCTCCACAGACATGACGCGCGGCGGAGAACTTANATACCCGCTC 490
OY 687 TTGCCAATGCGCGCTGACACACATTTCCNCCCAACNTCTTCTCCNTNGCCCTC 746
DB 491 TCTCGCGCGGCGGCTGATCATGATCCAGTACGTACCAACATCATCATCAACGCGCTC 550
OY 747 CACTCC 753
DB 551 CACTCC 557

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Job time : 1557 secs

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 11:17:55 ; Search time 181 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	778	96.5	806	19	AAV28655
2	591.8	73.4	748	20	AAV69457
3	591.2	73.3	745	20	AAV69450
4	588.8	73.1	793	20	AAV69447
5	572.2	71.0	727	19	AAV69460
6	543.8	67.5	727	19	AAV28658
7	536	66.5	724	19	AAV28660
8	510.8	63.4	704	20	AAV69446
9	496.8	61.6	706	20	AAV69458

10	169.4	21.0	1633	21	AAC36622	Arabidopsis thaliana
11	151	18.7	823	20	AAV69449	Banana fruit ripen
12	148.8	18.5	1526	21	AAC42069	Arabidopsis thaliana
13	144.4	17.9	749	20	AAV69445	Banana fruit ripen
14	142.8	17.7	842	19	AAV28659	Ripening banana pu
15	141.4	17.5	708	20	AAV69448	Banana fruit ripen
16	141	17.5	1521	21	AAC49440	Arabidopsis thaliana
17	134.6	16.7	687	19	AAV28656	Ripening banana pu
18	131.6	16.3	772	20	AAV69456	Banana fruit ripen
19	131	16.3	758	20	AAV69451	Banana fruit ripen
20	130.4	16.2	1233	21	AAC46041	Arabidopsis thaliana
21	130.4	16.2	1323	21	AAC51583	Arabidopsis thaliana
22	129.2	16.0	794	20	AAV69452	Banana fruit ripen
23	128.8	16.0	728	20	AAV69459	Banana fruit ripen
24	128.4	15.9	745	20	AAV69454	Banana fruit ripen
25	127	15.8	1779	21	AAC45923	Arabidopsis thaliana
26	126.2	15.7	731	20	AAV69455	Banana fruit ripen
27	124.6	15.5	1786	21	AAC40484	Arabidopsis thaliana
28	124	15.4	1440	20	AAC07385	Zinnia elegans pec
29	120.8	15.0	1359	21	AAC50766	Arabidopsis thaliana
30	119.4	14.8	710	20	AAV69453	Banana fruit ripen
31	118.4	14.7	1413	21	AAC51079	Arabidopsis thaliana
32	116.4	14.4	1257	21	AAC42899	Arabidopsis thaliana
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34	114.6	14.2	1514	21	AAC41563	Arabidopsis thaliana
35	113	14.0	1615	21	AAC51025	Arabidopsis thaliana
36	113	14.0	1617	21	AAC41994	Arabidopsis thaliana
37	110.4	13.7	1221	21	AAC47293	Arabidopsis thaliana
38	110.4	13.7	1631	21	AAC33659	Arabidopsis thaliana
39	110.4	13.7	1631	21	AAC49928	Arabidopsis thaliana
40	109.6	13.6	1125	21	AAC42903	Arabidopsis thaliana
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42	93.4	11.6	460	24	ABL93674	Plant microsatelli
43	83.4	10.3	1807	21	AAC51305	Arabidopsis thaliana
44	83.4	10.3	1812	21	AAC39116	Arabidopsis thaliana
45	81.8	10.1	1523	21	AAC51573	Arabidopsis thaliana

ALIGNMENTS

RESULT 1
AAV28655
AAV28655 strand; cDNA; 806 BP.
AAV28655:
29-JUL-1998 (first entry)
Ripening banana pulp cDNA clone U-068 SEQ ID NO:13.
Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;
genetic control; tissue senescence; ss.
Musa acuminata.
WO9811228-A2.
19-MAR-1998.
08-SEP-1997; 97WO-GB02424.
25-APR-1997; 97GB-0008366.
10-SEP-1996; 96GB-0018862.
(ZENEC) ZENECAL LTD.
Bird CR, Medina-Suarez RDJ, Seymour GB;
WPL: 1998-207389/18.
Modulation of ripening or tissue senescence in bananas - comprises
use of DNA isolated from ripening banana pulp to produce genetically

PT modified fruit
 XX
 PS Claim 1; Page 26; 72pp; English.
 XX
 CC The present sequence represents a cDNA clone isolated from ripening
 CC banana pulp. 57 clones were isolated and are given in AAV28643 to
 CC AAV28699. The cDNA clone sequences can be used in a method of modulating
 CC ripening or tissue senescence processes in plants of the genus *Musa*. The
 CC method comprises: (a) inserting into the plant material at least 1 of the
 CC 57 sequences (as above); (b) regenerating the plant material, and (c)
 CC selecting from the transformed regenerants, plants with modulated
 CC ripening or tissue senescence characteristics. Also described in the
 CC present invention are: (1) plants, their progeny, seed and material
 CC obtained from the plants, produced by the above method; (2) a vector
 CC functional in plants comprising a promoter region which is operably in
 CC plant cells, a polynucleotide sequence as defined above, and a
 CC transcription termination sequence; and (3) a method of controlling
 CC plant pathogens comprising the application of anti-pathogenic agent to
 CC plants of (1).
 XX
 SQ Sequence 806 BP; 157 A; 229 C; 212 G; 180 T; 28 other;

Query Match 96.5%; Score 778; DB 19; Length 806;
 Best Local Similarity 100.0%; Pred. No. 1e-221;
 Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTTCCTCCTTGATCACAATCTTTTGTCTGTGGAACGTGAGAGTGAGAGGCG 60
 DB 1 TGTTCCTCCTTGATCACAATCTTTTGTCTGTGGAACGTGAGAGTGAGAGGCG 60
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 QY 121 CTGTTTGAACGAGGTGCGGGGTGATTTGAAGGAGGAGGCTTCCTGCTGAGGAAT 180
 DB 121 CTGTTTGAACGAGGTGCGGGGTGATTTGAAGGAGGAGGCTTCCTGCTGAGGAAT 180
 QY 181 GCGGAGCATCGCGAGGACCTTGAGAGAGCCTCCGGAACCGAGCAGCGCGATGCT 240
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 DB 361 CTGTGCTGCGGTTCAGGCAACCCGATCGAGCTGTGCGGTGCGAGCCCTGATTTGGCAT 420
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 DB 421 GTCAAGAGAAAAAGCTCGCTGACTGCGGATTTGGCTTTGAGCGCAACGNAATNGTGGC 480
 QY 481 CCGGAGGGAATTTGTCTGTGACAGACTCCGGGAGCATGATCCCGGATATTC 540
 DB 481 CCGGAGGGAATTTGTCTGTGACAGACTCCGGGAGCATGATCCCGGATATTC 540
 QY 541 GCCCGGGAACACTTANATACCCGCTNTCCAAANGAAGTTGCCCTCTGGGATCCCTTT 600
 DB 541 GCCCGGGAACACTTANATACCCGCTNTCCAAANGAAGTTGCCCTCTGGGATCCCTTT 600
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 DB 601 AAACNMAANTGAAATCTCNCNANGAAGAACTCATTATGAAGCTTTAANCMAT 660
 QY 661 CGATGACNONGTCTCTGTCACATTTGCGATGCGGCTGNTACACNCAATTTCT 720
 DB 661 CGATGACNONGTCTCTGTCACATTTGCGATGCGGCTGNTACACNCAATTTCT 720

QY 721 TCCCAACNTCTTCTCCNTNGCCTCCNCTCCCAATGCAACCCCGGGAATTCCTNGT 780
 DB 721 TCCCAACNTCTTCTCCNTNGCCTCCNCTCCCAATGCAACCCCGGGAATTCCTNGT 780
 QY 781 CCCCNCTCCCTTCTCTATGATNG 806
 DB 781 CCCCNCTCCCTTCTCTATGATNG 806

RESULT 2
 AAV69457
 ID AAV69457 standard; cDNA; 748 BP.
 XX
 AC AAV69457;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Banana fruit ripening-related clone U-113 cDNA.
 XX
 KM Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KW triploid; plant breeding; ss.
 XX
 OS *Musa acuminata*.
 XX
 PN WO9853085-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-GB01297.
 XX
 PR 20-MAY-1997; 97GB-0010370.
 XX
 PA (ZENEC) ZENEC LTD.
 XX
 PI Bird CR, Medina-Suarez RDU, Seymour GB;
 XX
 DR WPI; 1999-059745/05.
 XX
 PT New method of modulating fruit ripening or tissue senescence
 PT characteristics of *Musa* plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics
 PS
 XX
 CC Claim 1; Page 29; 78pp; English.
 CC AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of *Musa*
 CC *acuminata* (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.
 XX
 SQ Sequence 748 BP; 154 A; 211 C; 206 G; 163 T; 14 other;

Query Match 73.4%; Score 591.8; DB 20; Length 748;
 Best Local Similarity 91.7%; Pred. No. 3.4e-166;
 Matches 664; Conservative 0; Mismatches 52; Indels 8; Gaps 4;

QY 1 TGTTCCTCCTTGATCACAATCTTTTGTCTGTGGAACGTGAGAGTGAGAGGCG 60
 DB 1 TGTTCCTCCTTGATCACAATCTTTTGTCTGTGGAACGTGAGAGTGAGAGGCG 60
 QY 16 TGTTCCTCCTTGATCACAATCTTTTGTCTGTGGAACGTGAGAGTGAGAGGCG 75
 DB 16 TGTTCCTCCTTGATCACAATCTTTTGTCTGTGGAACGTGAGAGTGAGAGGCG 75
 QY 61 GCATACGCGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 DB 61 GCATACGCGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 QY 76 GCATACGCGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 135
 DB 76 GCATACGCGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 135
 QY 121 CTGTTTGAACGAGAGTGTGCGGGGTGATTTGAAGGAGAGTCTCTGCTGAGGAAT 180
 DB 121 CTGTTTGAACGAGAGTGTGCGGGGTGATTTGAAGGAGAGTCTCTGCTGAGGAAT 180
 QY 136 CTGTTTGAACGAGAGTGTGCGGGGTGATTTGAAGGAGAGTCTCTGCTGAGGAAT 195
 DB 136 CTGTTTGAACGAGAGTGTGCGGGGTGATTTGAAGGAGAGTCTCTGCTGAGGAAT 195
 QY 181 GCGGAGCATCGCGAGAGCTTTGAGAGAGGCTCCGCGAAGCGAGCAGCGCCGATGCT 240

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Db      196 GCGGAGCATCGCGGAGGAGCTTGAGAGAGGCGCTCCGCAAGCGACGACGCCGATGCT 255
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Db      256 TCCCTTGAAGAGAGGCGCTTAACCCGGGAGCAGAAAGCCGACGTGACGACCCCGAGAG 315
QY      301 GTTGTGTCGAGCGTCTGTGATCAATCAACAGAGCGGCGGATGCTTGTGTAT 360
Db      316 GTTGTGTCGAGCGTCTGTGATCAATCAACAGAGCGGCGGATGCTTGTGTAT 375
QY      361 CTGTGTCGCTTCAAGCAACCCGATCGAGACTGTGCGGTGCGACCCCTGATTTGGCAT 420
Db      376 CTGTGTCGCTTCAAGCAACCCGATCGAGACTGTGCGGTGCGACCCCTGATTTGGCAT 435
QY      421 GTCAACAGAAAAAGCTCGCTACTGCGGCGATTTGGCTTTGAGCGACGACGATTTANGTGGC 480
Db      436 GTCAACAGAAAAAGCTCGCTACTGCGGCGATTTGGCTTTGAGCGACGATTTANGTGGC 495
QY      481 CGCGAGCGGGGAATTTGTGTGTGACAGACTCCGGGGACNATGATCCCGGAAATCCTTC 540
Db      496 CGCGAGCGGGGAATTTGTGTGTGACAGACTCCGGGGACNATGATCCCGGAAATCCTTC 555
QY      541 GCGCGGGGAACACTTANATACCCCGTCNTCCANGAAGTTGCCCTCTGTGGATCCCTTT 600
Db      556 CCGCGGGAACACTTANATACCCCGTCNTCCANGAAGTTGCCCTCTGTGGATCCCTTT 610
QY      601 AAACNCAANTGAATCTCNCNTCNANGAAGAACTCMTTATGAACAGCTTTAANAACNAT 660
Db      611 AAACNCAANTGAATCTCNCNTCNANGAAGAACTCMTTATGAACAGCTTTAANAACNAT 669
QY      661 CGATGACNCGTGTCTGCTGCACATTTGCCATGGCGCTGCTGNTCAACNCAANTTGN 720
Db      670 CGATGACNCGTGTCTGCTGCACATTTGCCATGGCGCTGCTGNTCAACNCAANTTGN 727
QY      721 TCCC 724
Db      728 CACC 731

RESULT 3
AAV69450
ID      AAV69450 standard; cDNA; 745 BP.
AC      AAV69450;
XX      15-MAR-1999 (first entry)
DE      Banana fruit ripening-related clone U-52 cDNA.
KW      Fruit ripening; banana; modulator; tissue senescence; crop; plant;
        triploid; plant breeding; ss.
OS      Musa acuminata.
XX      WO9853085-A1.
PN      26-NOV-1998.
XX      05-MAY-1998; 98WO-GB01297.
PF      20-MAY-1997; 97GB-0010370.
PR      (ZENBE) ZENECA LTD.
XX      PA
XX      Bird CR, Medina-Suarez RDJ, Seymour GB;
PI      WPI; 1999-059745/05.
DR      New method of modulating fruit ripening or tissue senescence
XX      characteristics of Musa plants - by introducing DNA sequences,
PT      useful in processes for modifying plant/fruit ripening
        characteristics

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XX      PS Claim 1; page 24-25; 78pp; English.
CC      CC AAV69440-v69512 are cDNA sequences which are used in a method to
XX      CC modulate the fruit ripening or tissue senescence characteristics of Musa
CC      CC acuminata (banana) plants. The method provides a recombinant way of
CC      CC modulating ripening/senescence characteristics of bananas, which are a
CC      CC globally important crop. In particular, the method can modulate such
CC      CC characteristics in the dessert banana, which due to its triploid nature
CC      CC is unaffected by conventional plant breeding techniques.
XX      SQ Sequence 745 BP; 153 A; 204 C; 203 G; 163 T; 22 other;
Query Match 73.3%; Score 591.2; DB 20; Length 745;
Best Local Similarity 90.5%; Pred. No. 5.2e-166;
Matches 673; Conservative 0; Mismatches 61; Indels 10; Gaps 5;
QY      1 TGTTCCTCTTCGATCAGATCTTTTGTCTGGAAGAGTGAGAGTGAGAGAGGCG 60
Db      7 TGTTCCTCTTCGATCAGATCTTTTGTCTGGAAGAGTGAGAGTGAGAGAGGCG 66
QY      61 GCAATGACGCGGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db      67 GCAATGACGCGGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 126
QY      121 CTGTGTTTGAAGGAGGTGCGGGGATGGAAGAGAGAGAGAGAGAGAGAGAGAGAT 180
Db      127 CTGTGTTTGAAGGAGGTGCGGGGATGGAAGAGAGAGAGAGAGAGAGAGAGAT 186
QY      181 GCGGAGCATTCGCGGAGGAGCTTGAAGAGAGGCTCCGCGACGACGACGCGCATGCT 240
Db      187 GCGGAGCATTCGCGGAGGAGCTTGAAGAGAGGCTCCGCGACGACGACGCGCATGCT 246
QY      241 TCCCTTGAAGAGAGGCTGTAAACCGGGGAGCAGAAAGCCGAGTGAGAGACCCGAGAG 300
Db      247 TCCCTTGAAGAGAGGCTGTAAACCGGGGAGCAGAAAGCCGAGTGAGAGACCCGAGAG 306
QY      301 GTTGTGAGCGGTCTGTATGAACATTAACAGAGAGGCGGCGAGATCTTGTGTAT 360
Db      307 GTTGTGAGCGGTCTGTATGAACATTAACAGAGAGGCGGCGAGATCTTGTGTAT 366
QY      361 CTGTGTCGCTTCAAGCAACCCGATCGAGACTGTGCGGTGCGACCCCTGATTTGGCAT 420
Db      367 CTGTGTCGCTTCAAGCAACCCGATCGAGACTGTGCGGTGCGACCCCTGATTTGGCAT 426
QY      421 GTCAACAG-AAAAAAGCTGCTGACTGCGGCAATTTGGCTTTGAGCGACGACGATTTANGTGG 479
Db      427 GTCAACAGAAAAAAGCTGCTGACTGCGGCAATTTGGCTTTGAGCGACGACGATTTANGTGG 486
QY      480 CGCGAGCGGGGAATTTGTGTGTGACAGACTCCGGGGACNATGATCCCGGAAATCCT 539
Db      487 CGCGAGCGGGG-ANTTGTATGCTGTGACAGACTCCGGGGACNATGAT-CCCGGAAATCCT 544
QY      540 CGCGCGGGAACACTTANATACCCGTCNTCCANGAAGTTGCCCTCTGTGGATCCCTT 599
Db      545 CMCOCGGGAACNCTTANATACCCGTCATCC-ANGACGTGCCCTCTGTGATCACTT 600
QY      600 TAAACNCAANTGAATCTCNCNTCNANGAAGAACTCMTTATGAACAGC---TTTANA 656
Db      601 TAAACNCAANTGAATCTCNCNTCNANGAAGAACTCMTTATGAACNCGCTTTNACA 660
QY      657 CNAATGATGACNCGTGTCTGCTGCACATTTGCCAATGGCGGCTGCTGACACNCAAT 716
Db      661 ACATGATGACCGCGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 720
QY      717 TTCNTCCCAACNCTTCTTCCNT 740
Db      721 TACATCAACAGATATCTCTCAT 744

RESULT 4
AAV69447
ID      AAV69447 standard; cDNA; 793 BP.

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XX AAV69447;
 AC 15-MAR-1999 (first entry)
 DT XX
 DE Banana fruit ripening-related clone U-22 cDNA.
 KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KM triploid; plant breeding; ss.
 XX
 OS Musa acuminata.
 XX
 PN W09853085-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-GB01297.
 XX
 PR 20-MAY-1997; 97GB-0010370.
 XX
 PA (ZENNE) ZENNECA LTD.
 XX
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;
 XX
 DR WPI; 1999-059745/05.
 XX
 PT New method of modulating fruit ripening or tissue senescence
 PT characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics
 XX.
 PS Claim 1; Page 22-23; 78pp; English.
 XX
 CC AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.
 XX
 SO Sequence 793 BP; 170 A; 222 C; 215 G; 171 T; 15 other;
 Query Match 73.1%; Score 588.8; DB 20; Length 793;
 Best Local Similarity 88.7%; Pred. No. 2.8e-165;
 Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;
 QY 1 TGTTCCTCTCTGATCATCTTTTGTCTCTGGAACCTGAGAGTGAAGAGCGG 60
 DB 8 TGTTCCTCTCTGATCATCTTTTGTCTCTGGAACCTGAGAGTGAAGAGCGG 67
 QY 61 GCAATGACGCGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTG 120
 DB 68 GCAATGACGCGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTG 127
 QY 121 CTGCTTTTGAACGAGGTCGGGGGTGATTTGAAGCGAGAGTCTCTGCTCGAGGAAT 180
 DB 128 CTGCTTTTGAACGAGGTCGGGGGTGATTTGAAGCGAGAGTCTCTGCTCGAGGAAT 187
 QY 181 GGGGAGCANTCGGGGAGAGCTTGAGAGAGGCTCCGCGAACCAGACCGCGGATGCT 240
 DB 188 GGGGAGCANTCGGGGAGAGCTTGAGAGAGGCTCCGCGAACCAGACCGCGGATGCT 247
 QY 241 TCCCTTGAAGAGAGGCTGTAACTCCGCGAGAGAGCCAGTCTGACGACCGCGGAGAG 300
 DB 248 TCCCTTGAAGAGAGGCTGTAACTCCGCGAGAGAGCCAGTCTGACGACCGCGGAGAG 307
 QY 301 GTTGTCTTCAAGGCTCTGATGACCATTAATCAACAGACGCGCTGACGATCTTTGTTAT 360
 DB 308 GTTGTCTTCAAGGCTCTGACGACCATTAATCAACAGACGCGCTGACGATCTTTGTTAT 367
 QY 361 CTGTCTGTGGGTTCAAGCAACCGATCGACGACTGCTGGCGGCGACCTGATTTGGCAT 420

DB 368 CTGTCTGTGGGTTCAAGCAACCGATCGACGACTGTGGGGTGGAGACCCCGATTGGCAT 427
 QY 421 GTCAACAG-AAAAAGCTCGCTGACCTGGCATTTGGCTTGGAGCAACGANTANGTG 479
 DB 428 GTCAACAGAAAAAGCTCGCTGACCTGGCATTTGGCTTGGAGCAACGANTANGTG 487
 QY 480 CCGGAGCGGGAATTTGTGTGTGACAGACTCCGGGAGACMATATCCCGTGAATCT 539
 DB 488 CCGGAGCGGAG-ANTTGTGTGTGTGACAGACTCCGGGAGAGATGCCGTGAATCTCTC 546
 QY 540 CGCCCGGAGACCTTAATATCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 599
 DB 547 GCGCGGGAACACTTAATATCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 602
 QY 600 TAAACNCAANTGGAATCTCNCCTCANGAGAGACTTATGACAGCTTTAANCA 659
 DB 603 TAAACNCAANTGGAATCTCNCCTCANGAGAGACTTATGACAGCTTTAANCA 660
 QY 660 TCGATGAGACNCGTGTCTGTCCACATTTGCCAATGGCGCTGTCCATCCAAATTTTC 719
 DB 661 TCGATGAGACCGG--TGTACAGTCCACATTTGCCAATGGCGCTGTCCATCCAA--TTA 717
 QY 720 NTCCCGCAACNTCTCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 777
 DB 718 ATCACCAACNTCTCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 777
 QY 778 NGTCCCGCTCCTCCT 792
 DB 778 TGTGCCACCTCTCT 792
 RESULT 5
 AAV69460 standard; cDNA; 727 BP.
 ID AAV69460
 AC AAV69460;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Banana fruit ripening-related clone U-139 cDNA.
 XX
 KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KM triploid; plant breeding; ss.
 XX
 OS Musa acuminata.
 XX
 PN W09853085-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-GB01297.
 XX
 PR 20-MAY-1997; 97GB-0010370.
 XX
 PA (ZENNE) ZENNECA LTD.
 XX
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;
 XX
 DR WPI; 1999-059745/05.
 XX
 PT New method of modulating fruit ripening or tissue senescence
 PT characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics
 XX
 PS Claim 1; Page 30-31; 78pp; English.
 XX
 CC AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature

CC Is unaffected by conventional plant breeding techniques.

XX Sequence 727 BP; 144 A; 199 C; 202 G; 157 T; 25 other;

Query Match 71.0%; Score 572.2; DB 20; Length 727;
Best Local Similarity 90.9%; Pred. No. 2.4e-160;
Matches 653; Conservative 0; Mismatches 57; Indels 8; Gaps 5;

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QY 1 TGTTCCTCTCTGATCAGATCTTTTGTCTGGGAAGGTGAGAGTGAAGAGGGG 60
DB 16 TGTTCCTCTCTGATCAGATCTTTTGTCTGGGAAGGTGAGAGTGAAGAGGGG 75
QY 61 GCAATGACGCGGGGTTTAAGATGATGATCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 76 GCAATGACGCGGGGTTTAAGATGATGATCTCTCTCTCTCTCTCTCTCTCTCT 135
QY 121 CTGCTTTTGAACGAGAGTGGGGGTGATTTGAGAGGAGAGTCTCTGAGAGAT 180
DB 136 CTGCTTTTGAACGAGAGTGGGGGTGATTTGAGAGGAGAGTCTCTGAGAGAT 195
QY 181 GGGGAGCATCGCGGAGGAGCTTGAAGAGGCTCCGCGAAGCGGAGCGGATGCT 240
DB 196 GGGGAGCATCGCGGAGGAGCTTGAAGAGGCTCCGCGAAGCGGAGCGGATGCT 255
QY 241 TCTTTGAAGAGAGGCTGTAAACCGGAGAGAGAGCGGATGAGAGAGAGAG 300
DB 256 TCTTTGAAGAGAGGCTGTAAACCGGAGAGAGAGAGCGGATGAGAGAGAGAG 315
QY 301 GTTGTCTGACGCTCTCTGATGACATTAATCAACAGACAGGCTGAGATCTTGT 360
DB 316 GTTGTCTGACGCTCTCTGATGACATTAATCAACAGACAGGCTGAGATCTTGT 375
QY 361 CTGTGCTGGGTTGACAGCAACCGATGACAGAGTGTGGGGTGGGA-CCGTGAT 419
DB 376 CTGTGCTGGGTTGACAGCAACCGATGACAGAGTGTGGGGTGGGA-CCGTGAT 435
QY 420 TGTCAACAGAAAAAAGCTGCTGACTGCGGATTTGGTGGAGCAGACGATTA 479
DB 436 TGTCAACAGAAAAAAGCTGCTGACTGCGGATTTGGTGGAGCAGACGATTA 495
QY 480 CCGGAGCGGGGAATTTGTTGTTGTGACAGACTCCGGGAGCAGATTAATCC 539
DB 496 CCGGAGCGGGGAATTTGTTGTTGTGACAGACTCCGGGAGCAGATTAATCC 554
QY 540 CCGGAGCGGGGAATTTGTTGTTGTGACAGACTCCGGGAGCAGATTAATCC 599
DB 555 CCGGAGCGGGGAATTTGTTGTTGTGACAGACTCCGGGAGCAGATTAATCC 610
QY 600 TAAACNANANTGGAATCTCNCNTCANANGAAGAACTTATGACAGCTTAANA 659
DB 611 TAAACNANANTGGAATCTCNCNTCANANGAAGAACTTATGACAGCTTAANA 669
QY 660 TCGATGACNCTGCTCTGCTGACATTTGCCAATGCGCGCTGCTGACCAAT 717
DB 670 TCGATGACNCTGCTCTGCTGACATTTGCCAATGCGCGCTGCTGACCAAT 726
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RESULT 6
AAV28658
ID AAV28658 standard; cDNA; 727 BP.
XX AAV28658;
XX 29-JUL-1998 (first entry)
DE Ripening banana pulp cDNA clone U-089 SEQ ID NO:16.
XX Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;
KM genetic control; tissue senescence; ss.
XX Musa acuminata.
XX WO9811228-A2.
PN

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XX 19-MAR-1998.  
PD 08-SEP-1997; 97MO-GB02424.  
PF 25-APR-1997; 97GB-0008366.  
PR 10-SEP-1996; 96GB-0018862.  
XX (ZENECALTD.)  
PA Bird CR, Medina-Suarez RDJ, Seymour GB;  
PI WPI; 1998-207389/18.  
DR Modulation of ripening or tissue senescence in bananas - comprises  
XX use of DNA isolated from ripening banana pulp to produce genetically  
PT modified fruit  
PS Claim 1; Page 28; 72pp; English.  
XX The present sequence represents a cDNA clone isolated from ripening  
CC banana pulp. 57 clones were isolated and are given in AAV28643 to  
CC AAV28699. The cDNA clone sequences can be used in a method of modulating  
CC ripening or tissue senescence process in plants of the genus Musa. The  
CC method comprises: (a) inserting into the plant material at least 1 of the  
CC 57 sequences (as above); (b) regenerating the plant material; and (c)  
CC selecting from the transformed regenerants, plants with modulated  
CC ripening or tissue senescence characteristics. Also described in the  
CC present invention are: (1) plants, their progeny, seed and material  
CC obtained from the plants, produced by the above method; (2) a vector  
CC functional in plants comprising a promoter region which is operably in  
CC plant cells; a polynucleotide sequence as defined above; and a  
CC transcription termination sequence; and (3) a method of controlling  
CC plant pathogens comprising the application of anti-pathogenic agent to  
CC plants of (1).  
XX  
SQ Sequence 727 BP; 145 A; 205 C; 196 G; 159 T; 22 other;  
Query Match 67.5%; Score 543.8; DB 19; Length 727;  
Best Local Similarity 86.8%; Pred. No. 7e-152;  
Matches 628; Conservative 0; Mismatches 91; Indels 6; Gaps 4;
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QY 2 GTTCTCTCTCTGATCAGATCTTTTGTCTGGGAAGGTGAGAGTGAAGAGGGCG 61
DB 8 GTTCTCTCTCTGATCAGATCTTTTGTCTGGGAAGGTGAGAGTGAAGAGGGCG 67
QY 62 CAATGACGCGGGGTTTAAGATGATGATCTCTCTCTCTCTCTCTCTCTCTCT 121
DB 68 CAATGACGCGGGGTTTAAGATGATGATCTCTCTCTCTCTCTCTCTCTCTCT 127
QY 122 TGTGTTTGAACGAGAGTGGGGGTGATTTGGAAGCAGAGAGTCTCTGCTGA 181
DB 128 TGTGTTTGAACGAGAGTGGGGGTGATTTGGAAGCAGAGAGTCTCTGCTGA 187
QY 182 GCGGAGCATCGCGGAGAGAGTGTGAGAGAGGCTCCGCGAAGCGGAGCGGAT 241
DB 188 GCGGAGCATCGCGGAGAGAGTGTGAGAGAGGCTCCGCGAAGCGGAGCGGAT 247
QY 242 CTTTGAAGAGAGGCTGTAAACCGGAGCAGAGAGCGGATGAGAGAGCGGAT 301
DB 248 CTTTGAAGAGAGGCTGTAAACCGGAGCAGAGAGCGGATGAGAGAGCGGAT 307
QY 302 TTGCTTGAACGAGTCTGATGACATTAATCAACAGACGCGCTGCAATCTT 361
DB 308 TTGCTTGAACGAGTCTGATGACATTAATCAACAGACGCGCTGCAATCTT 367
QY 362 TGTGCTGCGGTTGAGCAACCGGATGAGAGAGTGTGGGGTGGAGAGCGGAT 421
DB 368 TGTGCTGCGGTTGAGCAACCGGATGAGAGAGTGTGGGGTGGAGAGCGGAT 427
QY 422 TCAACAGAAAAAAGCTGCTGACTGAGTGGGCTTTGG-ACGCAACGATTA 480
DB 428 TCAACAGAAAAAAGCTGCTGACTGAGTGGGCTTTGG-ACGCAACGATTA 487
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xx	Sequence	724 BP; 143 A; 201 C; 197 G; 155 T; 28 other:
sq	Query Match	66.5%; Score 536; DB 19; Length 724;
	Best Local Similarity	89.7%; Pred. No. 1.5e-149;
	Matches 617; Conservative	0; Mismatches 62; Indels 9; Gaps 5
QY	6 TCTCCTTCGATCACAATCTTTTTCGCTCTCTGGGAAACGTGAGAGTGAAGACGAGGCGGCAT	65
Db	9 TCTCCTTCGATCACAATCTTTTTCGCTCTGGGAAACGTGAGAGTGAAGACGAGGCGGCAT	68
QY	66 GACGCGGGCTTAAAGATGGATTTCCCTCCCTGCTTTCTTCTTCGCGGCTTCCTGCTGAT	125
Db	69 GACGCGGGCTTAAAGATGGATTTCCCTCCCTGCTTTCTTCTTAAGGCTTCCTGCTGAT	128
QY	126 TTTCACAGGAGGCTGGGGGCTGGATTGGAAGCAGAGGCTCTTGCGCTTCAGAGAAATGCGG	185
Db	129 TTTCACAGGAGGCTGGGGGCTGGATTGGAAGCAGAGGCTCTTGCGCTTCAGAGAAATGCGG	188
QY	186 AGCATCCGCGAGGAGCTTGAAGAGAGGCTCCGCGCAAGCGACAGCGCGGATGCTTCTT	245

RESULT	8
AAV69446	
ID	AAV69446 standard; CDNA, 704 BP.
XX	
AC	
AAV69446;	
XX	
DT	15-MAR-1999 (first entry)
DE	
XX	Banana fruit ripening-related clone U-12 CDNA.
KW	Fruit ripening; banana; modulator; tissue senescence; crop; plant.
KW	triploid; plant breeding; ss.
XX	
OS	Musa acuminata.
XX	
PN	W09853085-A1.
XX	

Db 187 GCGGACATCCGAGAGAGCTTGAGAGAGCCCTCCGGAAAGCGGACCGCGGATGCTT 246
QY 242 CCTTGAAGAGAGGGCTGTATACCCGGGACAGAGCCGAGTGCAGACGCCGAGAGG 301
Db 247 CCTTGAAGAGAGGGCTGTATACCGAGGACAGAGCCGNNCTACCTACCCGAGAGG 306
QY 302 TTGCTTGAGAGGCTCTGTAGATCATATATCAACAGACGGCTCGAGATCTTGGTTATC 361
Db 307 TTGCTTGAGAGGCTCTGTAGATCATATCAACAGACGGCTCGAGATCTTGGTTATC 366
QY 362 TGTGCGGGTTAGGCAA-CCGATCGAGACTGCGGGGGTGG-CGACCCGTATGGCA 419
Db 367 TGTGCGGGTTAGGCAACCCGATCGAGACTGCGGGGGTGG-CGACCCGTATGGCA 426
QY 420 TGTCAACAGAAAAAGCTGCTGACTGCGGCAATTGGC-TTGGAGCGCAACGNAATNGTG 478
Db 427 TGTCAACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGGCCGACANCGNAATNGTG 486
QY 479 GCGGC--GACGGGGAATTTGTTGCTTG-TCACAGACTCC-GGGGACNATGATCCCGTGA 534
Db 487 GCGGCGACCGGGGGAATTTGTTGTTGACANACTCCGGGGAGCATGATCCCGTGAA 546
QY 535 ATCCCTGCCC--GGGAACACTTANATACCCCGTCNCCANGAAGTTGCCCTCTGGGA 592
Db 547 ATCTCTCCCCGGGGAACACTTANATATNCNCCGTCATCCAGANGAGCTTGCCTCT--GGA 603
QY 593 TCCCTTTTAACNCNANATGGAATCTCNCNTNANGAAGAACTGTTATGACAGCTTT 652
Db 604 TCMCTTTTAACNCNANATGGAATATCACCCTCC-NNGAAAGACTCCTTATGAAGA-CTTT 661
QY 653 AANANATGAGTGAACNCNCTGCTCCTGTCACATTGCCAATGGC 697
Db 662 AANACATCAATGNCNCTGTCACGTCACATTTGCCNATGGC 706

RESULT 10
AAC36622 standard; DNA: 1633 BP.
AAC36622:
AC AAC36622:
XX
XX
DT 17-OCT-2000 (first entry)
XX
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14477.
XX
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX
PR 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123548.
PR 23-MAR-1999; 9905-0125788.
PR 29-MAR-1999; 9905-0126264.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129645.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130449.
PR 23-APR-1999; 9905-0130510.
PR 28-APR-1999; 9905-0130891.
PR 30-APR-1999; 9905-0131449.
PR 9905-0132048.

PR 30-APR-1999; 9905-0132407.
PR 04-MAY-1999; 9905-0132484.
PR 05-MAY-1999; 9905-0132485.
PR 06-MAY-1999; 9905-0132486.
PR 07-MAY-1999; 9905-0132487.
PR 11-MAY-1999; 9905-0132863.
PR 14-MAY-1999; 9905-0134256.
PR 14-MAY-1999; 9905-0134218.
PR 14-MAY-1999; 9905-0134219.
PR 14-MAY-1999; 9905-0134221.
PR 14-MAY-1999; 9905-0134370.
PR 18-MAY-1999; 9905-0134768.
PR 19-MAY-1999; 9905-0134941.
PR 20-MAY-1999; 9905-0135124.
PR 21-MAY-1999; 9905-0135353.
PR 24-MAY-1999; 9905-0135629.
PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136392.
PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137222.
PR 03-JUN-1999; 9905-0137528.
PR 04-JUN-1999; 9905-0137502.
PR 07-JUN-1999; 9905-0137724.
PR 08-JUN-1999; 9905-0138094.
PR 10-JUN-1999; 9905-0138540.
PR 14-JUN-1999; 9905-0138847.
PR 16-JUN-1999; 9905-0139119.
PR 17-JUN-1999; 9905-0139453.
PR 18-JUN-1999; 9905-0139492.
PR 18-JUN-1999; 9905-0139454.
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PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139817.
PR 22-JUN-1999; 9905-0139899.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 01-JUL-1999; 9905-0142154.
PR 02-JUL-1999; 9905-0142055.
PR 06-JUL-1999; 9905-0142390.
PR 08-JUL-1999; 9905-0142803.
PR 09-JUL-1999; 9905-0142920.
PR 12-JUL-1999; 9905-0142977.
PR 13-JUL-1999; 9905-0143452.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144085.
PR 16-JUL-1999; 9905-0144325.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.
PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 19-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
PR 20-JUL-1999; 9905-0144684.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.

PR	21-JUL-1999	9905-0145088
PR	22-JUL-1999	9905-0145085
PR	22-JUL-1999	9905-0145087
PR	22-JUL-1999	9905-0145089
PR	22-JUL-1999	9905-0145192
PR	23-JUL-1999	9905-0145145
PR	23-JUL-1999	9905-0145218
PR	23-JUL-1999	9905-0145224
PR	26-JUL-1999	9905-0145276
PR	27-JUL-1999	9905-0145313
PR	27-JUL-1999	9905-0145518
PR	27-JUL-1999	9905-0145519
PR	28-JUL-1999	9905-0145551
PR	02-AUG-1999	9905-0146388
PR	02-AUG-1999	9905-0146386
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PR	03-AUG-1999	9905-0147038
PR	04-AUG-1999	9905-0147204
PR	04-AUG-1999	9905-0147302
PR	05-AUG-1999	9905-0147192
PR	05-AUG-1999	9905-0147260
PR	06-AUG-1999	9905-0147303
PR	06-AUG-1999	9905-0147416
PR	09-AUG-1999	9905-0147935
PR	10-AUG-1999	9905-0148171
PR	11-AUG-1999	9905-0148171
PR	12-AUG-1999	9905-0148341
PR	13-AUG-1999	9905-0148565
PR	13-AUG-1999	9905-0149684
PR	16-AUG-1999	9905-0149368
PR	17-AUG-1999	9905-0149175
PR	18-AUG-1999	9905-0149426
PR	20-AUG-1999	9905-0149722
PR	20-AUG-1999	9905-0149829
PR	20-AUG-1999	9905-0149923
PR	23-AUG-1999	9905-0149302
PR	23-AUG-1999	9905-0149330
PR	25-AUG-1999	9905-0150566
PR	26-AUG-1999	9905-0150084
PR	27-AUG-1999	9905-0150865
PR	27-AUG-1999	9905-0151066
PR	30-AUG-1999	9905-0151080
PR	30-AUG-1999	9905-0151303
PR	31-AUG-1999	9905-0151338
PR	01-SEP-1999	9905-0151330
PR	07-SEP-1999	9905-0152363
PR	10-SEP-1999	9905-0153750
PR	13-SEP-1999	9905-0153758
PR	15-SEP-1999	9905-0154018
PR	16-SEP-1999	9905-0154039
PR	22-SEP-1999	9905-0154179
PR	22-SEP-1999	9905-0155139
PR	23-SEP-1999	9905-0155486
PR	24-SEP-1999	9905-0156589
PR	28-SEP-1999	9905-0156588
PR	29-SEP-1999	9905-0156596
PR	04-OCT-1999	9905-0157117
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PR	06-OCT-1999	9905-0157865
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PR	14-OCT-1999	9905-0159329
PR	14-OCT-1999	9905-0159330
PR	14-OCT-1999	9905-0159331
PR	14-OCT-1999	9905-0159637
PR	14-OCT-1999	9905-0159638
PR	18-OCT-1999	9905-0159584
PR	21-OCT-1999	9905-0160741

PR	21-OCT-1999;	99SUS-0160767
PR	21-OCT-1999;	99SUS-0160770
PR	21-OCT-1999;	99SUS-0160778
PR	21-OCT-1999;	99SUS-0160814
PR	21-OCT-1999;	99SUS-0160815
PR	22-OCT-1999;	99SUS-0160981
PR	22-OCT-1999;	99SUS-0160981
PR	22-OCT-1999;	99SUS-0160981
PR	22-OCT-1999;	99SUS-0161004
PR	25-OCT-1999;	99SUS-0161405
PR	25-OCT-1999;	99SUS-0161405
PR	25-OCT-1999;	99SUS-0161405
PR	26-OCT-1999;	99SUS-0161359
PR	26-OCT-1999;	99SUS-0161359
PR	26-OCT-1999;	99SUS-0161361
PR	28-OCT-1999;	99SUS-0161361
PR	28-OCT-1999;	99SUS-0161362
PR	28-OCT-1999;	99SUS-0161393
PR	28-OCT-1999;	99SUS-0161393
PR	29-OCT-1999;	99SUS-0162142

Query Match	21.08;	Score 169.4;	DB 21;	Length 1633;
Best Local Similarity	63.58;	Pred. No. 4.6e-40;		
Matches 304; Conservative	0;	Mismatches 168;	Indels 7;	Gaps 4;

274 GAAGCCGAGTCGACGACCCCGAGGAGGTGCTTCGACGGTCTGATGACCATAACAAC 333

Db 243 GAACATGCAGTGAAGACCAGATGAAGTCCGCTGCCATGGTGGACATGAGCATTGGAAC 302

334 AGCACGGCTGCAGATCTCTGGTTATCTGTCTGCGGTTCAAGCAACCGATCGAC 393

Db 303 AGCACAGAGCGGAGAAGATTAGGTTACTTCTCCTGCGCCACCGGCAACCCAATCGACGAT 362

394 TCCTGGCGGTGCGACCTGATTGGCATGTCAACAGAAAAAGCTCGCTGACTGGGCATT 453

Db 363 TGCTGGCGTTGGCGACCGCAATGGCAGCTCCGTCGCAACGTTTAGCCGATTGCTCAATC 422

QY 454 GGCTTTGGACGCAACGCNATANGTGGCCCGACGGGGAATTTGTTCCGTTGTGACAGACTC 513

DB 423 GGATTTCGCCGCAACGCCAATCGGAGGCCGCGAC-GGTCTTTCACGTCGTAACCGACCC 481

514 C G G G A C N A T G A T C C C C G T G A A T C C T C G C C C G G A A C A C T T A N A T A C C C C G T C N I C C A A N 5/3

DD 40Z 180906ALCCGAI-LCCG1IMAILCCCAIACCGGAAACILCCGICAGCCLCGIGAILC --- 331

[illegible][illegible][illegible]

694 TGGCGCGCTGCTNTCACCANCCAAATTTCNTCCCGCAACNTCTTCCTTCCGCTNTGCGCGCTCCNCTGC 752

db 656 TGGAGCTTGCTCAGGATTCATACGTTAGGACATTATTGTCATGGGATTCATGTC 714

RESULT 11	1
AAV69449	1

ID	Standard; cDNA; 823 bp.
XX	

AC AAV09449;
XX

U1 13-MAY-1999 (first entry)
XX

bandana tunic xpepnting related clothe o 21 cdnna.

KW triplod; plant breeding; ss.

OS Musa acuminata.

PN	WO9853085-A1.	
XX		

PD 26-NOV-1998.
XX
XX 05-MAY-1998; 98MO-GB01297.
XX
PR 20-MAY-1997; 97GB-0010370.
XX
XX (ZENE) ZENECA LTD.
XX
PI Bird CR, Medina-Suarez RDJ, Seymour GB;
XX
DR WPI; 1999-059745/05.
XX
XX New method of modulating fruit ripening or tissue senescence
PT characteristics of Musa plants - by introducing DNA sequences,
PT useful in processes for modifying plant/fruit ripening
PT characteristics
XX
XX Claim 1; Page 24; 78pp; English.
XX
XX AAV69440-V69512 are cDNA sequences which are used in a method to
CC modulate the fruit ripening or tissue senescence characteristics of Musa
CC acuminate (banana) plants. The method provides a recombinant way of
CC modulating ripening/senescence characteristics of bananas, which are a
CC globally important crop. In particular, the method can modulate such
CC characteristics in the desert banana, which due to its triploid nature
CC is unaffected by conventional plant breeding techniques.
XX
XX Sequence 823 BP; 168 A; 266 C; 222 G; 150 T; 17 other;
SQ
Query Match 18.7%; Score 151; DB 20; Length 823;
Best Local Similarly 63.7%; Pred. No. 1,1e-34;
Matches 272; Conservative 0; Mismatches 149; Indels 6; Gaps 4;
OY 327 AATCAACAGCAGCGCTCGAGATCTCTGTTATCTGCTGCGGTTACGCAACCCGAT 386
DB 137 AAGCTTGACGCTTCGCGCGGCGGACTGGGCTTCTCTATGCGGACCGCAATCCGAT 196
OY 387 CGACGACTGCTGCGCGTGCAGCCCTGATTTGGCATGTCAACAGAAAAAGCTCGTACTG 446
DB 197 CGACGACTGCTGCGCGTGCAGCTCTGACTGCGCGCAACCGGAGCGGCTCGGACTG 256
OY 447 CGCATTTGCTTTGGAGCGACGACGCMATANGTGGCCCGGAGGGAATTTGTTGTTGTA 506
DB 257 CGCATTCGCGGTTTGCGGAAGACGCGATTGGGGGAGGAGCGCG -AGATATAGTGTGA 315
OY 507 CACACTCCGGGAGCMATGATCCCGTGAATCTCGCCCGGAGACACTTAATACCCGTC 566
DB 316 CCACAGCTGCGGAGCGACGACG -CCCCGTCAATCCGAGCGGCGCGCTCCGTAAGCCGTC 374
OY 567 NTCCAANGAAGTTGCCCTCTGCGATCCCTTTAAACNCAANTGGAATTCNCTCNA 626
DB 375 ATCCAGAGGAGGAGCCCGCTGT - - -GGATCATCTTCAAGCGGAGCATGTATC -CAGTTGA 430
OY 627 NGGAAGACTCNTTATGACAGCTTTAANCAATTCATGACACMCNGTGTCTGTCACA 686
DB 431 AGGAGAGGCTCATCATCACTCACTCCACAAGCCATCGACGCGCGGCGGCGGAGGTCACA 490
OY 687 TTGCGCATGGCGGCTGCTGNTCAACCAACCAATTTNTGCCCAACMTCTTCCMNGCCTC 746
DB 491 TCTCCGGCGGCGGCTGATCATCCATCCACTACGTCACCAATCATCATCAAGGCGTC 550
OY 747 CMCCTCC 753
DB 551 CACATCC 557
RESULT 12
AAC42069
ID AAC42069 standard; DNA; 1526 BP.
XX
XX AAC42069;
XX
DT 17-OCT-2000 (first entry)

XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34171.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123160.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0139119.
PR 14-JUN-1999; 99US-0139847.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999: 99US-0139817.
PR 22-JUN-1999: 99US-0139899.
PR 23-JUN-1999: 99US-0140353.
PR 23-JUN-1999: 99US-0140354.
PR 24-JUN-1999: 99US-0140695.
PR 28-JUN-1999: 99US-0140823.
PR 29-JUN-1999: 99US-0140991.
PR 30-JUN-1999: 99US-0141287.
PR 01-JUL-1999: 99US-0141842.
PR 01-JUL-1999: 99US-0142154.
PR 02-JUL-1999: 99US-0142055.
PR 06-JUL-1999: 99US-0142390.
PR 08-JUL-1999: 99US-0142803.
PR 09-JUL-1999: 99US-0142920.
PR 12-JUL-1999: 99US-0142977.
PR 13-JUL-1999: 99US-0143542.
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PR 16-JUL-1999: 99US-0144085.
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PR 19-JUL-1999: 99US-0144335.
PR 20-JUL-1999: 99US-0144352.
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PR 20-JUL-1999: 99US-0144884.
PR 21-JUL-1999: 99US-0144814.
PR 21-JUL-1999: 99US-0145086.
PR 21-JUL-1999: 99US-0145088.
PR 22-JUL-1999: 99US-0145085.
PR 22-JUL-1999: 99US-0145087.
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PR 22-JUL-1999: 99US-0145192.
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PR 26-JUL-1999: 99US-0145276.
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PR 27-JUL-1999: 99US-0145918.
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PR 02-AUG-1999: 99US-0146389.
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PR 23-AUG-1999: 99US-0149930.
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PR 26-AUG-1999: 99US-0150884.
PR 27-AUG-1999: 99US-0151065.
PR 27-AUG-1999: 99US-0151066.

PR 27-AUG-1999: 99US-0151080.
PR 30-AUG-1999: 99US-0151303.
PR 31-AUG-1999: 99US-0151438.
PR 01-SEP-1999: 99US-0151930.
PR 07-SEP-1999: 99US-0152363.
PR 10-SEP-1999: 99US-0153070.
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PR 15-SEP-1999: 99US-0154018.
PR 16-SEP-1999: 99US-0154039.
PR 20-SEP-1999: 99US-0154779.
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PR 23-SEP-1999: 99US-0155486.
PR 24-SEP-1999: 99US-0155659.
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PR 07-OCT-1999: 99US-0158029.
PR 08-OCT-1999: 99US-0158232.
PR 12-OCT-1999: 99US-0158369.
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PR 13-OCT-1999: 99US-0159294.
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PR 14-OCT-1999: 99US-0159329.
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PR 14-OCT-1999: 99US-0159637.
PR 14-OCT-1999: 99US-0159638.
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PR 25-OCT-1999: 99US-0161405.
PR 25-OCT-1999: 99US-0161406.
PR 26-OCT-1999: 99US-0161359.
PR 26-OCT-1999: 99US-0161360.
PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161820.
PR 28-OCT-1999: 99US-0161992.
PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.

Query Match 18.5%; Score 148.8; DB 21; Length 1526;
Best Local Similarity 58.9%; Pred. No. 6,3e-34;
Matches 285; Conservative 1; Mismatches 192; Indels 6; Gaps 3;

OY 274 GAAGCCGACGTGCACACCCGAGAGGTGCTTCGACGCTCCTGATGACATATCAAC 333
DB 203 GAACATGCACTTGAGATGACAGAGAGTACGCTCATGCTCAACCGAATTCATCGACAT 262
OY 334 AGCAGCGCTCGCAGATCTCTGTTATCTGCTGCGGTTACAGCAACCGATCGACGAC 393
DB 263 AGCAGACGAGAGAGATGATAGATCTCTCATGCTCAACCGAATTCATCGACAT 322
OY 394 TCGTGGCGGTGCGACCTTGATTTGGCATGTGCACAGAAAAAGTCTGCTGACGCGCAT 453
DB 323 TGTGGCGGTGCTGATGAGATGCGCAATCCGCGAAAAATCATTCACCAATTCGCAATC 382
OY 454 GCGTTGACGACCAACCNATANGTGGCGCGACGAGGGAATTTGTTGTTGACAGACTC 513
DB 383 GCGTTGCGTCGCAACCAATCGAGGCGGACGAC-GGTCGTTACTAGCTAGTGTGACCC 441
OY 514 CCGGACNATGATCCCGGTGAATCTCGCCCGGGAACACTTANATACCCCGCTNCTCAAN 573
DB 442 AAACGACGATTAACCCGTTAATTCCTTAACCGGGAACATTAAGTCAACGCAATTAACG 501

QY 574 GAACTGCCCCCTCTGGATCCCTTTAAACNCAANTGAAATCTCNCNANGAGA 633
 Db 502 AA---GAACCATATGATGATGCTTTAAAGCATGATGTCATATAA- TTAAGAAAGA 556
 QY 634 ACTGNTATGACAGCTTTAANACNATGATGACNCGTCTCTGTCACATTCGCA 693
 Db 557 ACTATGATGAAAGCTTCAAAACATGATGTCGTGGCCTCAACGTTCAATAGCTAA 616
 QY 694 TGGCGCTGCTGACCAACCAATTTCTCCCAACNTCTCTCCNCTGCTCCGCTCC 753
 Db 617 TGGTGCATGATACGATTCAGTTGCTGACTACATTAATCAATGAGGATTCATTTCA 676
 QY 754 CAAT 757
 Db 677 TGAT 680
 RESULT 13
 AAV69445
 ID AAV69445 standard; cDNA; 749 BP.
 AC AAV69445;
 XX 15-MAR-1999 (first entry)
 DE Banana fruit ripening-related clone U-11 cDNA.
 KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KM triploid; plant breeding; ss.
 OS Musa acuminata.
 PN WO9853085-A1.
 PD 26-NOV-1998.
 PF 05-MAY-1998; 98WO-GB01297.
 PR 20-MAY-1997; 97GB-0010370.
 PA (ZENECA LTD.
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;
 DR WPI; 1999-059745/05.
 XX New method of modulating fruit ripening or tissue senescence
 PT characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics
 PS Claim 1; Page 21-22; 78pp; English.
 CC AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the dessert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.
 CC
 XX Sequence 749 BP; 157 A; 245 C; 197 G; 128 T; 22 other;
 SQ
 Query Match 17.9%; Score 144.4; DB 20; Length 749;
 Best Local Similarity 64.0%; Pred. No. 9.4e-33;
 Matches 275; Conservative 0; Mismatches 147; Indels 8; Gaps 5;

Db 195 ATCGACGACTGCTGGCGGTGCGACCTGACAGGCGTGAACAACGCGAGCGGCTGAC 254
 QY 445 TGGCGCATTTGGCTTTGGACGACGACNATANGTGGCGCGCGGGAATTTGTTGT 504
 Db 255 TGGCCCATCGGCTTGGGAGACGCGCTTTGGGGGCGAGGCGCG-AGATATACNTGCT 313
 QY 505 GACAGACTCCGGGACNATGATCCCGTGAATCTCGCGCGGGAACACTTANATACCGG 564
 Db 314 GACGACAGATGGGACGACGACN-CCCCGTCATCGGAAGGCGGACGCTCGGTAACGGC 372
 QY 565 TCTTCCAAANGAAGTTGCCCTCTGGGATCCCTTTAAACNCAANTGAAATCTCCTC 624
 Db 373 TCATCC---AGGAGGAGCCGCTGTGATCATCTTCAAGCGCGACATGTCATCCACTG 428
 QY 625 NANGAAGAA-CCTGNTATGACAGCTTTAANACNATGATGACNCGTCTGCTGTC 683
 Db 429 AAGAGAGAACTCATGATGAACTCCACACAGACATGAGCGCGGCGCGAGCGTC 488
 QY 684 ACATTGCCAATGGCGCTGCTGACCAACCAATTTCTCCCAACNTCTTCTCCNTNGC 743
 Db 489 ACATCTCGGGGCGCGCTGGATCAGCATCC-AGTACGTCACCAACATCCTCATCCAGGC 547
 QY 744 CTCGCTGCC 753
 Db 548 GTCCACATCC 557
 RESULT 14
 AAV28659
 ID AAV28659 standard; cDNA; 842 BP.
 AC AAV28659;
 XX 29-JUL-1998 (first entry)
 DE Ripening banana pulp cDNA clone U-U115 SEQ ID NO:17.
 KW Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;
 KM genetic control; tissue senescence; ss.
 OS Musa acuminata.
 PN WO9811228-A2.
 PD 19-MAR-1998.
 PF 08-SEP-1997; 97WO-GB02424.
 PR 25-APR-1997; 97GB-0008366.
 PR 10-SEP-1996; 96GB-0018862.
 PA (ZENECA LTD.
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;
 DR WPI; 1998-207389/18.
 XX Modulation of ripening or tissue senescence in bananas - comprises
 PT use of DNA isolated from ripening banana pulp to produce genetically
 PT modified fruit
 PS Claim 1; Page 28-29; 72pp; English.
 CC The present sequence represents a cDNA clone isolated from ripening
 CC banana pulp. 57 clones were isolated and are given in AAV28643 to
 CC AAV28659. The cDNA clone sequences can be used in a method of modulating
 CC ripening or tissue senescence processes in plants of the genus Musa. The
 CC method comprises: (a) inserting into the plant material at least 1 of the
 CC 57 sequences (as above); (b) regenerating the plant material, and (c)
 CC selecting from the transformed regenerants, plants with modulated
 CC ripening or tissue senescence characteristics. Also described in the
 CC present invention are: (1) plants, their progeny, seed and material

CC obtained from the plants, produced by the above method; (2) a vector
 CC functional in plants comprising a promoter region which is operably in
 CC plant cells, a polynucleotide sequence as defined above, and a
 CC transcription termination sequence; and (3) a method of controlling
 CC plant pathogens comprising the application of anti-pathogenic agent to
 CC plants of (1).

XX Sequence 842 BP; 177 A; 277 C; 218 G; 154 T; 16 other;

Query Match 17.7%; Score 142.8; DB 19; Length 842;
 Best Local Similarity 64.3%; Pred. No. 3e-32;
 Matches 276; Conservative 0; Mismatches 144; Indels 9; Gaps 5;

Qy 325 ATAAATCAACAGCAGCGCTCGAGATCTTGTGTTATCTGTCGCGGTTCAAGCAACCG 384
 Db 140 AGAAGCTGGAACGCTGTCGGCGCGGCGACTGGGCTTACTGTATGGGCGACCGCAATCCG 199
 Qy 385 ATCGACGACTGCTGGCGGTGCGACCTGATGGCATGTCAACAGAAAAAGCTGCTGAC 444
 Db 200 ATCGACGACTGCTGGCGGTGCGACCTGATGGCATGTCAACAGCGGCGGCTGCTGAC 259
 Qy 445 TCGCGCATTTGCTTTGGACGCAAGCNAATANGTGGCCGCGACGGGGAATTTGTTGTTGT 504
 Db 260 TCGCGCATTTGCTTTGGACGCAAGCNAATANGTGGCCGCGACGGGGAATTTGTTGTTGT 318
 Qy 505 GACAGACTCGCGGAGCNAATGATCCCGGATCCGCGCGGGAACACTTANATACCCCG 564
 Db 319 GACGAGAGTGGCGGAGCNAATGATCCCGGATCCGCGCGGGAACACTTANATACCCCG 377
 Qy 565 TCNTCCAAAGAGTTGCCCTCTGGGATCCCTTTAAACNCAATGAAATCTCNCCTC 624
 Db 378 TCATCC---AGGAGGAGCCGCTGTGATCATCTTCAAGCGGACATGTGTCATCCAGCT 432
 Qy 625 NANGAAGAACTCMTTATGAAACAGCTTTAANCAATGATGACNCGTGTCTGTCGA 684
 Db 433 GAAGAGAGAGTCTATCATGAACCTCCACAGACCATGACGCGGCGGCGACGAGGTCCA 492
 Qy 685 CATTGCAATGAGCGCTGCTCANTCACCANCAATTTTCCCAACATCTTCTTCCTNCGC 744
 Db 493 CATCTCGGCGGCGGCGGCTGATCACCACC--AGTACGTACCAACATCATCTCCACGGCG 550
 Qy 745 TCCTCTCCG 753
 Db 551 TCACATCC 559

RESULT 15

AAV69448 standard; cDNA: 708 BP.

AC AAV69448;

XX 15-MAR-1999 (first entry)

DE Banana fruit ripening-related clone U-31 cDNA.

KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KW triploid; plant breeding; ss.

XX Musa acuminata.

XX MO9853085-A1.

XX 26-NOV-1998.

XX 05-MAY-1998; 98WO-GB01297.

XX 20-MAY-1997; 97GB-0010370.

XX (ZENE) ZENECA LTD.

XX Bird CR, Medina-Suarez RDJ, Seymour GB;

DR WPI; 1999-059745/05.

XX New method of modulating fruit ripening or tissue senescence
 PT characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics

XX Claim 1; Page 23; 78pp; English.

CC AAV69440-v69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.

XX Sequence 708 BP; 140 A; 225 C; 192 G; 134 T; 17 other;

Query Match 17.5%; Score 141.4; DB 20; Length 708;
 Best Local Similarity 60.3%; Pred. No. 7.2e-32;
 Matches 290; Conservative 0; Mismatches 182; Indels 9; Gaps 5;

Qy 325 ATAAATCAACAGCAGCGCTCGAGATCTTGTGTTATCTGTCGCGGTTCAAGCAACCG 384
 Db 137 AGAAGCTGGAACGCTGTCGGCGCGGCGACTGGGCTTACTGTATGGGCGACCGCAATCCG 196
 Qy 385 ATCGACGACTGCTGGCGGTGCGACCTGATGGCATGTCAACAGAAAAAGCTGCTGAC 444
 Db 197 ATCGACGACTGCTGGCGGTGCGACCTGATGGCATGTCAACAGCGGCGGCTGCTGAC 256
 Qy 445 TCGCGCATTTGCTTTGGACGCAAGCNAATANGTGGCCGCGACGGGGAATTTGTTGTTGT 504
 Db 257 TCGCGCATTTGCTTTGGACGCAAGCNAATANGTGGCCGCGACGGGGAATTTGTTGTTGT 315
 Qy 505 GACAGACTCGCGGAGCNAATGATCCCGGATCCGCGCGGGAACACTTANATACCCCG 564
 Db 316 GACGAGAGTGGCGGAGCNAATGATCCCGGATCCGCGCGGGAACACTTANATACCCCG 374
 Qy 565 TCNTCCAAAGAGTTGCCCTCTGGGATCCCTTTAAACNCAATGAAATCTCNCCTC 624
 Db 375 TCATCC---ANGAGGAGCCGCTGTGATCATCTTCAAGCGGACATGTGTCATCCANCTG 430
 Qy 625 NANGAAGAACTCMTTATGAAACAGCTTTAANCAATGATGACNCGTGTCTGTCGA 684
 Db 431 GAAGAGAGAGTCTATCATGAACCTCCACAGACCATGACGCGGCGGCGACGAGGTCCA 490
 Qy 685 CATTGCAATGAGCGCTGCTCANTCACCANCAATTTTCCCAACATCTTCTTCCTNCGC 743
 Db 491 CATCTCGGCGGCGGCGGCTGATCACCACC--AGTACGTACCAACATCATCTCCACGGCG 550
 Qy 744 CTCCTCNC--TCCCAATGCAACCCCGGGAATTTCTCTGTCCTCCCTCTCTCTATG 801
 Db 551 GTCCACATTCACAGATGCAATTCACANGGCGGGAATCTCTGTCGACATCCCATG 610
 Qy 802 G 802
 Db 611 G 611

Search completed: June 19, 2003, 12:46:56
 Job time : 184 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 11:40:35 ; Search time 1102 Seconds
(without alignments)
11845.338 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806
Sequence: 1 TGTCTCTCCTCATGACACA.....TCCCTCTCTCTATGATNG 806

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlin:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_estl3:*
13: gb_estl4:*
14: gb_estl5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	23.0	501	9	A1770665
2	176	21.8	480	9	A1770665
3	173.6	21.5	589	17	A2135244
4	170	21.1	595	14	B0741525
5	169.2	21.0	462	17	BH874844
6	166	20.6	800	14	BQ999911

7	165	20.5	720	14	BQ870176
8	164.4	20.4	784	17	A2916009
9	162.4	20.1	685	14	BQ795866
10	150	18.6	632	13	B1959076
11	149.4	18.5	679	10	AV822011
12	149.2	18.5	883	10	BE035831
13	144.8	18.0	612	14	B0148154
14	143.8	17.8	420	14	B0134100
15	141.2	17.5	518	14	B0104182
16	141	17.5	365	12	BF655654
17	140.2	17.4	634	14	AM223193
18	139.8	17.3	789	10	BG599600
19	138.8	17.2	541	10	AM398301
20	133.8	16.6	632	14	B0148911
21	130.4	16.2	541	10	AV527067
22	130.2	16.2	542	12	BG040772
23	130	16.1	629	10	AV827058
24	129.6	16.1	620	10	AV825500
25	126.6	15.7	539	10	AV527181
26	126.4	15.7	579	10	AV442702
27	126.4	15.7	727	14	BQ634030
28	125.8	15.6	362	10	AV420958
29	124.4	15.4	635	14	BQ700242
30	124.2	15.4	609	17	BH717800
31	123.6	15.3	515	14	BQ634633
32	122.4	15.2	672	12	B1924648
33	122.4	15.2	686	14	BQ401767
34	122.4	15.2	876	12	BG441931
35	121.4	15.1	764	17	BH583673
36	120.4	14.9	436	12	BG319625
37	120.2	14.9	786	17	BH647126
38	119.4	14.8	605	12	BG045860
39	117.4	14.6	666	12	BG599297
40	117.4	14.6	773	14	BQ508106
41	116	14.4	728	14	BQ699768
42	115.4	14.3	473	13	BM492945
43	115	14.3	546	12	BF008833
44	114.8	14.2	644	10	AM683073
45	114	14.1	567	13	B1471247

ALIGNMENTS

RESULT 1
LOCUS A1770665
DEFINITION 606055G03.x2 606 - Ear tissue cDNA library from Schmidt lab Zea
mays CDNA, mRNA sequence.
ACCESSION A1770665
VERSION A1770665.1 GI:5268701
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 606055 row: G column: 03.
Location/Qualifiers
1..501
/organism="Zea mays"

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/cultivar="Ohio43"
/db_xref="taxon:4577"
/clone_1lb="606 - Ear tissue cDNA library from Schmidt
lab"
/tissue_type="mixed"
/dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XJOLR (Stratagene)"
/notes="Organ: Immature ear; Vector: pBR-CMV; Site_1: EcORI
; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt
lab"

BASE COUNT      111 a 178 c 137 g 75 t
ORIGIN
Query Match      23.0%; Score 185; DB 9; Length 501;
Best Local Similarity 69.2%; Pred. No. 8.7e-45;
Matches 306; Conservative 0; Mismatches 128; Indels 8; Gaps 5;

OY 312 GGTCTGATGACATATACACAGCAGCGCTCGAGATCTCTGTTATCTGTCGCGG 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6 GCTCTCAGGTCTCATCAACACATCAAGCCCGCGGAAATCTCGGTACTGTGCGG 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 372 TTGAGCAACCCGATGACGAGCTGCGGCTGCGACCCGATGATGCGATGCAACAGAA 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 66 GACAGGCAACCCGATGACGAGCTGCGGCTGCGACCCGATGATGCGATGCGACAGCAACCGGAA 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 432 AAAGCTGCTGACTGCGGCAATGCTTGGACGCAACGCAATANGTGGCCGCGACGCGGA 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 126 GCGCTGCGGCACTGTGGCATCGCTTGGCCGCAACGCCATCGGCGCGGTGAC -GGCA 184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 492 ATTGTCTGTTGACAGACTCGGCGGACATATCCCGTGAATCTGCGCCGCGGAGCA 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 185 AGATCTACGTGTGACCGGACCGGAGGATGACA -CCGTGTCAACCGCGCAAGGCGACC 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 552 CTTANATACCCGCTCTGTCANANGAATGCGCCCTGCGATCCCTTAAACNCAANT 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 244 CTCCGCTAGCGCTCATCCAGGAA ----GAGCGGCTGTGATCATCTTCAAGGGGACAT 299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 612 GGAATCTCNCCTNANGAAGAACTNTATGAACGCTTTAANACNATGATGACNEN 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 300 GGTCATCAGCGCTC -AAGGAGGAGACTCATCATGAACGCTTCAAGACCATGACGAGCGG 358
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 672 GTGTCTGTCGTCATGTCGAATGGCGGCTGTCACGCAATTCNCCGCAACNCC 731
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 359 GCGCAACGTGCACATCGCCATGTCCTGATCACCATCC -AGTACATACCAACGTC 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 732 TTCTTCNTNGCCTCCNCTCCC 753
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 418 ATCATCCACGGGCTCCACATCC 439
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
AJ469163      480 bp      mRNA      linear      EST 24-MAY-2002
LOCUS      AJ469163      S00008 Hordeum vulgare cDNA clone S0000800244H10F1, mRNA
DEFINITION      sequence.
ACCESSION      AJ469163
VERSION      AJ469163.1 GI:21185119
KEYWORDS      EST.
SOURCE      Hordeum vulgare.
ORGANISM      Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 480)
; Title: Hordeum.
Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
Barley EST's
Unpublished (2002)
Contact: Schulman AH
Institute of Biotechnology
University of Helsinki
P.O. Box 56 (Valkinkari 6A), University of Helsinki FIN-00014,
Finland. Location/Qualifiers

FEATURES

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source
1. .480
/organism="Hordeum vulgare"
/db_xref="taxon:4513"
/clone_1lb="S0000800244H10F1"
/tissue_type="Callus"
/notes="Callus K19"

BASE COUNT      102 a 175 c 134 g 69 t
ORIGIN
Query Match      21.8%; Score 176; DB 9; Length 480;
Best Local Similarity 68.2%; Pred. No. 4.5e-42;
Matches 300; Conservative 0; Mismatches 132; Indels 8; Gaps 5;

OY 314 TCTGATGACCAATATCAACAGCAGCGCTCGAGATCTTGGTTATCTGTCGCGTT 373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 14 TGCTCAGGTGATCAGGACAGCAGCCCGGAGAACCTGGGGTACTCTGTCGGCA 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 374 CAGGCAACCCGATGACGAGCTGTGGGCTGCGACCCGATGATGCAAGAAAA 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 74 CCGGGAACCCCATGATGATGCTGCGGCTGCGACTGCGACACAAACCGGACAG 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 434 AGCTCGTACGCGGATGCTTGGTGGACGCAACGCAATANGTGGCGCGAGGGGANT 493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 134 GCTTCGCGGACCTGCGCATGCTTGGCCGCAACGCCATCGGCGCGGAC -GGCAAG 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 494 TTGTCTGTTGACAGACTCGGCGGACATGATCCCGTGAATCTCGCCGCGGAACT 553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 193 ATCTAGTGTGCTACTGACGCGGCGGACAGCA -CCCCGTGAACCCCAAGAGGACCT 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 554 TATATACCCGCTCTCCANANGAAGTTGCCCTCTGCGGATCCCTTAAACNCAANT 613
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 252 GCGCTACGCGGCTCATCC ---AGGAGAGAGCGCTGTGATCATCTTCAAGCGGACATG 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 614 AATCTCNCNANGAAGAACTNTATGAACGCTTTAANACNATGATGACNEN 673
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 308 TCATCACCTC -AGCCAGGAGCTATGATGAAGCTTCAAGACCATGCGCGCGG 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 674 GTCTGTCGACATGTCGAATGGCGCTGTCACGCAATTCNCCGCAACNCTT 733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 367 GCCACGTGACATGCGCAACGCGCGCTGATCACCATCC -ATTAGTGCACCAAGCTCAT 425
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 734 CTTCNNTNGCCTCCNCTCCC 753
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 426 CATCCAGGCGCTGACATCC 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
A2135244      589 bp      DNA      linear      GSS 02-JUN-2000
LOCUS      A2135244      OSJNB0115A18r CUGI Rice BAC Library (EcORI) Oryza sativa genomic
clone OSJNB0115A18r, DNA sequence.
ACCESSION      A2135244
VERSION      A2135244.1 GI:8214537
KEYWORDS      GSS.
SOURCE      Oryza sativa.
ORGANISM      Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.
1 (bases 1 to 589)
; Title: A BAC End Sequencing Framework to Sequence the Rice Genome
Wing, R.A. and Dean, R.A.
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACGCTATGACCATG
Class: BAC ends

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High quality sequence start: 21
High quality sequence stop: 547.
Location/Qualifiers
1. 589

/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="OSJNB0115A18r"
/clone_lib="CUCI Rice BAC Library (EcoRI)"
/tissue_type="leaf"
/lab_host="E. coli DH10B"

/note="Vector: pBACindigo; site_1: EcoRI; site_2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."

BASE COUNT 121 a 203 c 171 g 3 others
ORIGIN

Query Match 21.5%; Score 173.6; DB 17; Length 589;
Best Local Similarity 68.1%; Pred. No. 2,7e-41;
Matches 297; Conservative 0; Mismatches 131; Indels 8; Gaps 5;

OY 314 TCCGTGATGACATTAATCAACAGACGCTCGAGATCTTGTATCTGTCGGGTT 373
DB 1 TCATCAGGTGATCGAGACACGACGCGAGAGAGCTGCTGCTGCGGCA 60
OY 374 CAGGCAACCGGATGACGATGCTGCGGCTGAGACCTGATGCGATGCAACGAAAA 433
DB 61 CCGGCAATCGATCGACGATCTGAGGTGACCCGGAGTGGCAAGAAATCGCCAGC 120
OY 434 AGCTGCTGACTGCGGATGCTTGGACGACGATATGATGCGCGGAGGAT 493
DB 121 GGCTGGCGGATCGGCGATCGGCTTGGCGGCAACCCATCGCGCGCGGAC 179
OY 494 TTGTTGTTGTGACAGACTGCGGGGACATCCCGTGAATCCTGCGCGGAGACT 553
DB 180 ATCTGCTGTGTCACGACGACCCGACGACGACGACGACGACGACGACGCT 238
OY 554 TANAATACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
DB 239 CCGGTACGCGCTATCC---GCGAGACGCGCTGCTGCTGCTGCTGCTGCTGCT 294
OY 614 AATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
DB 295 TGATCAGGCTC--AAGCAGAGAGCTGATGATGATGATGATGATGATGATGATGAT 353
OY 674 GTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 733
DB 354 GCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 412
OY 734 GTTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 749
DB 413 CATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428

RESULT 4
LOCUS B0741525
DEFINITION B0741525, 595 bp, mRNA, linear, EST 17-JUL-2002
B0741525.1 GI:21888312
similar to TR:024416 024416 PECTATE LYASE, mRNA sequence.
ACCESSION B0741525
VERSION B0741525.1
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max

REFERENCE 1 (bases 1 to 595)
Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna, A., Bolla, B., Matra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, R., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available through: Resgen, Invitrogen Corp, 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact: c@resgen.com web site: www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 430.

FEATURES
source

1. 595
Location/Qualifiers
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID:"
/clone_lib="Gm-cl045"
/tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"
/lab_host="DH10B"

/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 149 a 171 c 169 g 106 t
ORIGIN

Query Match 21.1%; Score 170; DB 14; Length 595;
Best Local Similarity 63.7%; Pred. No. 3.3e-40;
Matches 307; Conservative 0; Mismatches 168; Indels 7; Gaps 4;

OY 236 ATGCTTCTTGAAGAGAGGCTGTAACCCGGGACAGACCCGAGTGAACCCCG 295
DB 117 ATTGCGAATGGCAGAAAGGTGAGGAGGCTTGAATGAATGACATGATGATGATGAT 176
OY 296 AGGAGTCTTCTGACGCTGCTGATGACATATATCAACGACGCGCTGCAATCTTGG 355
DB 177 AGGAAATGCTTCTTCACTGTTGATGAGAGATACGAACTACACGCGCTGCAAGAACTGGA 236
OY 356 GTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 415

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
RESULT 8 A2916009	784 bp DNA linear GSS 15-MAR-2001	A2916009	A2916009	GI:13347280	Zea mays. Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.	
REFERENCE	Missouri Maize Project--Maize Mapping Project. PstI_1_Zea mays B73 PstI leaf tissue library Unpublished (2001)					
AUTHORS	Missouri Maize Project--Maize Mapping Project University of Missouri 209 Curtis Hall, Columbia, MO 65211, USA Tel: 573 882 8214 Fax: 573 884 7850 Email: sschroeder@celephais.agron.missouri.edu					
COMMENT	Class: shotgun; Location/Qualifiers					
FEATURES	Source					
	1..784 /organism="Zea mays" /cultivar="B73" /db_xref="taxon:4577" /clone_lib="Maize PstI B73 Leaf" /russ_type="Leaf" /lab_host="DH5 alpha" /note="Organ: Leaf; Vector: PUC19; PstI digested B73 genomic sucrose gradient size fractionated fragment sizes of 0.5kb to 2kb ligated to PUC19 transformed in DH5 alpha"					
BASE COUNT	190 a 202 c 210 g 182 t					
ORIGIN						
Query Match	20.4%; Score 164.4; DB 17; Length 784; Best Local Similarity 70.0%; Pred. No. 1.9e-38;					
Matches	266; Conservative 0; Mismatches 107; Indels 7; Gaps 4;					
QY	319 ATGACATATCAACAGACGCGCTGCGACATCTTGGTATCTGTGTCGTGCGTTACGGC 378					
DB	412 AGGTCCATCAAGAAAGACGACGCGCCCGGGAACCTCGGTACTGTGCGGACAGCGC 471					
QY	379 AACCGATGACGACTGCTGCGGTGGGACGCCCTATGCGCATGTCAACAGAAAAAGCTC 438					
DB	472 AACCGATGACGACTGCTGCGGTGGGACGCCCTATGCGCATGTCAACAGAAAAAGCTC 531					
QY	439 GCTGACTGCGCATTTGGCTTTGGAGCGCAACGCNATANGTGCGCGCGAGGGGAATTTGTT 498					
DB	532 GCGCATGCGGCATCTGGGTTGGCGCGCAAGCCATTCGGCGCGCGCGAC -GCCAAGGTGTA 590					
QY	499 CGTTGTGACAGACTTCGGGGACNATGATCCCGTGATCTCTGCGCGCGGGAACACTTANAT 558					
DB	591 CGTGTGACGAGCCCGAGCGACGACGAT -CCGTGAAGCCCGCGGAGGACACCTCTCGGC 649					
QY	559 ACCCGGTCNCCCANGAAGTTGCCCTCTGGATGCCCTTTAAACNMANNTGGAATC 618					
DB	650 ACCGCGTCATCC ---AGGAGAGACCGCGTGTGATCATCTTCAAGCGGAGCATGTGTC 705					
QY	619 TCNCTCANAAGAAACACTNTTATGAACAGCTTAAANACNATGATGAGCNCNCTGCTT 678					
DB	706 ACCTG -GAGGAGAGAGCTCATCATGAACAGCTTCAAGACCATTCAGAGGCGCGGCCCA 764					
QY	679 CGTCCACATTCGCCAATGGCG 698					
DB	765 CGTCCACATTCGCCAATGGCG 784					

LOCUS	BO795866	685 bp	mRNA	linear	EST 30-JUL-2002
DEFINITION	EST 4804 Ripening Grape berries Lambda zap II Library Vitis vinifera cDNA clone RT021D12 3', mRNA sequence.				
ACCESSION	BO795866				
VERSION	BO795866.1	GI:22010832			
KEYWORDS	EST.				
SOURCE	Vitis vinifera.				
ORGANISM	Vitis vinifera				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.				
AUTHORS	1 (bases 1 to 685) Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Bartieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Gillsant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.				
TITLE	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Romieu C. Unité de Recherche des Produits de la Vigne Institut National de la Recherche Agronomique 2, place Viala, 34 060 Montpellier Cedex 01, France Tel.: 00-33-(0)4-99-61-28-63 Fax: 00-33-(0)4-99-61-28-57 Email: romieu@ensam.inra.fr Seq primer: 77.				
FEATURES	Location/Qualifiers				
source	1..685 /organism="Vitis vinifera" /cultivar="Shiraz" /db_xref="taxon:29760" /clone="RT021D12" /clone_lib="Ripening Grape berries Lambda zap II library" /dev_stage="ripening stage" /note="Organ: Fruit; Vector: Lambda zap II; Site_1: Eco RI ; Site_2: XhoI; Oriented library, construction described in Generation of ESTs from grape Berry (skin, pulp or seeds) at various developmental stages by Terrier,N., Ageorges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158 (12): 1575-83 2001"				
BASE COUNT	171 a 166 c 180 g 168 t				
ORIGIN					
Query Match	20.1%; Score 162.4; DB 14; Length 685;				
Best Local Similarity	62.8%; Pred. No. 7.2e-38;				
Matches	297; Conservative 0; Mismatches 169; Indels 7; Gaps 4;				
OY	280 GCACTGCACACCCCGAGAGAGGTTGCTTCACGCTCGATGACCATATACAAGCACG 339				
DB					
OY	206 GCACTTATATGACCCAGATGACAGTGCTTCATGTGTGACATGACACATTCGGAGACCA 265				
DB					
OY	340 GCTCGAGATCTCTGGTTATCTGTCGCGGCGGTTCCAGACACCCGATCGACAGCTGCG 399				
DB					
OY	266 GAGGAAAGGAATTAAGTTATTTCTCGTGTGAACCTGTAATCCCATTTGATGACTGCTGG 325				
DB					
OY	400 CGGTGCAGACCCCTGATTTGGCATGTCAACAGAAAAAAGCTCGCTGACTGGCGCATTTGGCTTT 459				
DB					
OY	326 CGATGTGACCAACAATTTGGCAAAAAGAACCGTAAGGCGCTTGCAGACTGGCGCATTTGGCTTT 385				
DB					
OY	460 GGACGCAACGCNATFANGTGGCGCGAGCGGGAATTTGTTGCTTGTGACAGACTCCGGGGA 519				
DB					
OY	386 GGGCAATATGCAATTTGAGAGCGCTGGA-TGGACGCTCTATGTGTGCTACACTCCCTGGTGA 444				
DB					
OY	520 CNAATGATCCCCGTAATCTCGCCCGGGAACACTTAANAATCCCGCTNTCCAAAGAAGTT 579				
DB					
OY	445 TGATGAT-CCGTGTAACCCCAAGCTGTGCACTTGCCGCCATGCTGTATCC----AGAT 499				
DB					
OY	580 GCCCCCTCTGGGATCCCTTTTAACNCNNAATGAATAATCTCNCNANGAAGAACTCNT 639				
DB					
OY	500 GCTCTCTCTGATTTGTGTTCAACGACGACATGTTGATCAACAT-GAAGACGAGAGCTCAT 558				
DB					
OY	640 TATGACAGGCTTTAANCAATCGATGACACNCNGTGTCTGTGTCACATTTGCCAATGGCGC 699				
DB					

Db	Accession	Definition	Version	Keywords	Source	Organism
Db	559	CATGACAGCGTCAAAACAATTGATGGCGCGGGGCTCAATGTCACATGTCATGAGC	618			
0y	700	CTGCTCACCACCAATTCCTTCCTCCCAACNTCTTCCTCCNTNGCCTCCNCTCC	752			
Db	619	ATGATCAGCAGCGTCAATTCGACGAAATGTATATATCATGCTGTCCACATCC	671			
RESULT 10						
LOCUS	B1959076					
ACCESSION	B1959076					
VERSION	B1959076.1					
KEYWORDS	GI:16310331					
SOURCE	EST.					
ORGANISM	Hordeum vulgare.					
	Hordeum vulgare					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae					
REFERENCE	1 (bases 1 to 632)					
AUTHORS	Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,					
	Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons					
	,J., Oates,R. and Main,D.					
	Development of a genetically and physically anchored EST resource					
	for barley genomics: Morex rachis cDNA library					
	Unpublished (2001)					
JOURNAL	Contact: Wing RA					
COMMENT	Clemson University Genomics Institute					
	100 Jordan Hall, Clemson, SC 29634, USA					
	Tel: 864 656 7288					
	Fax: 864 656 4293					
	Email: rwing@clemson.edu					
	Total hg bases = 473					
	Seq primer: AATTAACCTCCTCCTAAGG					
	High quality sequence stop: 613.					
FEATURES	Location/Qualifiers					
source	1..632					
	/organism="Hordeum vulgare"					
	/cultivar="Morex"					
	/db_xref="taxon:4513"					
	/clone="HVSME0018A17f"					
	/clone_id="Hordeum vulgare rachis EST library HVCNMA0015					
	(normal)"					
	/tissue_type="Rachis"					
	/lab_host="TJ0121"					
	/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:					
	XhoI; Plants were grown at Washington State University,					
	Pullman, WA in a greenhouse, the rachises were excised and					
	frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close					
	lab at the University of California, Riverside total RNA					
	was prepared, poly(A) was purified, one primary					
	unamplified cDNA library was made, and 1 million pfu were					
	in vivo excised to give pBluescript SK(-) cDNA phagemids					
	(Chin). Phagemids were plated and picked at the Clemson					
	University Genomics Institute (CUGI) (Begum, Palmer,					
	Frisch, Atkins and Wing). Plasmid DNA preparations, DNA					
	sequencing and sequence analysis were performed at CUGI					
	(Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The					
	sequence has been trimmed to remove vector sequence and					
	contains a minimum of 100 bases of phred value 20 or					
	above. For more details on library preparation and					
	sequence analysis see					
	http://www.genome.clemson.edu/projects/barley. To order					
	this clone see http://www.genome.clemson.edu/orders Also					
	see Close TJ, Wing R, Kleinhofs A, Wise R (2001)					
	Genetically and physically anchored EST resources for					
	barley genomics. Barley Genetics Newsletter 31:29-30.					
	(http://wheat.pw.usda.gov/ggpages/bgr/31/cover.html)"					
BASE COUNT	125 a	246 c	171 g	89 t	1 others	

Query Match	18.68;	Score 150;	DB 13;	Length 632;
Best Local Similarity	67.28;	Pred. No. 4e-34;		
Matches 254;	Conservative	0;	Mismatches 117;	Indels 7;
				Gaps 4
QY	376	GGCAACCCGATCGACGACTGCTGGCGGCGCACCCCTGATGTGGCATGTCAACAGAAAAAG	435	
Db	11	GGGAACCCCATCGACGACTGCTGGCGGCGCACCTGAGCATGTGGCAACAAACCGGAGGCG	70	
QY	436	CTGCGTACGTCGGGCATTTGGCTTTGGACGCAACGCMATANGTGGCCGCGACGGGGAATTT	495	
Db	71	CTGCGCCACACTGGGCATCGGCTTTGGCGCGCAACGCCATCGCGCGCGCGAC--GGCAAAAT	129	
QY	496	GTTTGCTGTGACAGACTCCGGGGGACNATGATCCCGGTGAATCCCTCGCCGGGAAACACTTA	555	
Db	130	CTAGCTGTGTCACGACGACGCGGGCGACGACGACCCGGGAGAGACCCCAAGAAAGGACCTCTGC	189	
QY	556	NATACCCCGTCNCCCAANGAAGTTGCCCCCTCTGGGATCCCCCTTTAAACNMAANTGAA	615	
Db	190	GCTACGCGCGTCATCC---AGGAGAGCGCGCTGTGATCATCTCAACCGGACATGGTC	245	
QY	616	ATTCNCTCMANNGSAAAGACNCTTATGAACAGTTTPAANCNMTGATGACNONGGT	675	
Db	246	ATCACCCCTC--AGCCAGGAGCTCATATGAAAGCTTCAAGACCATCGACGGCCCGGGCGC	304	
QY	676	CCTGTCACGATTTGCCAATGGCGGCGCTGNCACANCCAAATTTCTTCCCAACNTCTTT	735	
Db	305	CAAGGTCAACATTCGCCAAGGCGGCGCTGACCAACCATCC--AGTAGTCACCAAGACATCA	363	
QY	736	TTCNTNCCCTCNCNCTCCC	753	
Db	364	TTCACGGCGTCCACATCC	381	

```

RESULT 11
AV822011
LOCUS          679 bp      mRNA      linear      EST 01-APR-2002
DEFINITION     AV822011 RAF14 Arabidopsis thaliana cDNA clone RAF104-19-N09 5',
                mRNA sequence.
ACCESSION      AV822011
VERSION        AV822011.1
KEYWORDS       GI:19864043
SOURCE         EST-
               thale cress.
ORGANISM       Arabidopsis thaliana
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1 (bases 1 to 679)
AUTHORS        Seki,M., Natusaka,M., Ishida,J., Kamiya,A., Setou,M., Nakajima,M.,
                Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
                Arakawa,T., Shibata,K., Shingawa,A., Muramatsu,M., Hayashizaki,Y.
                and Shinozaki,K.
                Large scale analysis of Arabidopsis full-length cDNA (2002p)
                Unpublished (2002)
TITLE          Contact: Motoaki Seki
JOURNAL        Plant Functional Genomics Research Group
COMMENT        RIKEN Genomic Sciences Center
                3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                Tel: 81-298-36-4359
                Fax: 81-298-36-9060
                Email: mseki@rtc.riken.go.jp
                An Arabidopsis full-length cDNA library was constructed essentially
                as reported previously (Seki et al., 1998). This clone is in a
                modified pBluescript vector as a SsrI/XhoI insert. Please visit our
                web site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for
                further details.

FEATURES
             source
             Location/Qualifiers
             1..679
             /organism="Arabidopsis thaliana"
             /db_xref="taxon:3702"
             /clone="RAF104-19-N09"
             /clone_lib="RAF14"
             /dev_stage="rosette plants"

```



```

/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF062C07FL"
/tissue_lib="Developing flower"
/dev_stage="Developmentally pooled. Contains a mixture of
very young, developing, fully-opened flowers and flowers
in early transition into pods."
/notes="Vector: lambda zap; cDNA was prepared from polyA+
enriched, pooled samples of equivalent amounts of total
RNA from very young, developing, fully-opened flowers and
flowers transitioning into pods. The cDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-Zap XR vector
using ExAssist helper phage and the E. coli strain
XL1-Blue MRF' (Stratagene). Excised plasmids were plated
using SOLR cells."
BASE COUNT      176 a      107 c      158 g      171 t
ORIGIN
Query Match      18.0%; Score 144.8; DB 14; Length 612;
Best Local Similarity 57.4%; Pred. No. 1.5e-32;
Matches 294; Conservative 0; Mismatches 211; Indels 7; Gaps 3;

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OY 246 GGAGAGAGGGCTGAACCCGGGCGAGCAAGCCGCAATCGACGACCCCGAGAGGTTGC 305
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 25 GGAAGAACACGCTGGAATTTGAATGACGCTGCTGCTGCTAATCCAAAAGAGGTGGC 84
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 306 TTCGACGCTCTGATGATCAATCAACAGCAGGCTCGAGATCTTGGTTATCTGTC 365
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 85 TTCTATGTTGATGATGACATCCAGACAGTACTGAAGAGATCTTGGATTTTCTC 144
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 366 GTGGGTTGAGCAACCCGATGACGACTGCTGGCGGTGACACCTGATGGCATGCA 425
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 145 GTGTGGAACCGGTAACTTATGATGCTGGCGGTGACACCTGATGGCATGCA 204
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 426 CAGAAAAAGCTGCTGACGCTGGGCTTTGGAGCAACGCAATGAGGCGCGGA 485
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 205 CAGGAGGCTGTAGACAGCTGTTGTTGGTGAAGAACGCAATGGGCGCGGA 264
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 486 CGGGAAATTTGCTGTGACAGACTCCGGGGAAGATGATCCCGTGAATCTGCGCG 545
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 265 -TGGAAGTACTATGTTGTCACTGACGCCAAGAGATGATGA-CCCTGTTAACCTGAGCA 322
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 546 GGAACATTANATACCCCGTCNTCCANAGAGTTGCCCTCTGGGATCCCTTTAAACN 605
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 323 GGAACCTTGGCGCCAGCGCTTATCCAGATAG-----ACCACTTTGATTTGTTCAAGA 377
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 606 CNAANTGGAATTCNCNCNNGAAGAACTNTTATGACAGCTTTAANACNATGATG 665
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 378 GAGACATGTTATTCAGTTTAAACAGAGCTTATTTGTAACAGTTTCAAGCAATTTGATG 437
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 666 GACNCGTCTCTGTCATGATGCGGCTGCTGNTCAACCAACCAATTTCTCCCC 725
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 438 GAGAGGAGCTAATGTCATATTTGCTAATGAGAGGTCATATCTTATGATGTTACTA 497
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 726 AACNTCTTCTTCNTNCGCTCCNCTGCCCAAT 757
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 498 ATGTTATCATTCATGAGTCTTCATATTCATGAT 529
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RESULT 14
LOCUS      B0134100      420 bp      mRNA      linear      EST 19-APR-2002
DEFINITION      sat57c10.y1 Gm-c1052 Glycine max cDNA clone SOYBEAN CLONE ID:
                  Gm-c1052-3596 5' similar to TR:024416 024416 PECTATE LYASE. ;, mRNA
sequence.      B0134100.
ACCESSION      B0134100.1 GI:20208011
KEYWORDS      EST.
SOURCE      soybean.

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ORGANISM      Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 420)
REFERENCE
AUTHORS      Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
A., Bolla,B., Merritt,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
Y., Peterson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurr
R., Riller,E., Kohn,S., Shiu,T., Jackson,Y., Cardenas,M., McCann
R., Waterston,R. and Wilson,R.
TITLE      Public Soybean EST Project
JOURNAL      Unpublished (1999)
COMMENT      Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314.286.1800
Fax: 314.286.1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: c@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco.
FEATURES
source
location/Qualifiers
1..420
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1052-3596"
/tissue_lib="Gm-c1052"
/dev_stage="1 week old"
/label="DHI0B"
/notes="Vector: pBluescript II SK+; Site.1: EcoRI; Site.2:
XhoI; The Harosoy NIL was constructed and seed was
provided by Dr. J. Specht, University of Nebraska
(Shoemaker and Specht, 1995). The cDNA library was
constructed from mRNA isolated from whole seedlings of 1
week old greenhouse grown plants. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site and a 3'
anchor. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by XhoI digestion. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(GibcoBRL). The library was constructed in cooperation
with Dr. Paul Kelm's laboratory at Northern Arizona
University."
BASE COUNT      112 a      88 c      118 g      102 t
ORIGIN
Query Match      17.8%; Score 143.8; DB 14; Length 420;
Best Local Similarity 63.2%; Pred. No. 2.4e-32;
Matches 270; Conservative 0; Mismatches 150; Indels 7; Gaps 4;

```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 12:43:50 ; Search time 46 Seconds

(Without alignments)
5373.510 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806
Sequence: 1 TGTCTCTCCTTCGATGCACA.....TCCCTCTCTCTATGATG 806

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued_Patents_NA:*
1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
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4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/1/ina/CTUS.COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by the result to have a score greater than or equal to the score of the change being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.6	6.9	1170	3	US-08-467-023-94
2	55.2	6.8	1337	3	US-08-467-023-1
3	54	6.7	1278	3	US-08-467-023-96
4	46.6	5.8	1328	1	US-08-290-448A-58
5	46.6	5.8	1328	1	US-08-290-448A-58
6	46.6	5.8	1328	1	US-08-175-069A-58
7	46.6	5.8	1328	4	US-08-461-939B-58
8	46.6	5.8	1328	4	US-08-461-939B-58
9	46.6	5.8	1349	1	US-08-290-448A-73
10	46.6	5.8	1349	1	US-08-290-448A-73
11	46.6	5.8	1349	1	US-08-175-069A-73
12	46.6	5.8	1349	4	US-08-461-939B-73
13	46.6	5.8	1349	4	US-08-461-939B-73
14	46.6	5.7	7218	4	US-08-232-463-14
15	43.8	5.4	1320	1	US-08-290-448A-75
16	43.8	5.4	1320	1	US-08-290-448A-75
17	43.8	5.4	1320	1	US-08-175-069A-75
18	43.8	5.4	1320	4	US-08-461-939B-75
19	43.8	5.4	1320	4	US-08-461-939B-75
20	41.8	5.2	1160	1	US-08-290-448A-77
21	41.8	5.2	1160	1	US-08-290-448A-77
22	41.8	5.2	1160	4	US-08-175-069A-77
23	41.8	5.2	1160	4	US-08-461-939B-77
24	41.8	5.2	1160	4	US-08-461-939B-77
25	38.8	4.8	1196	1	US-08-290-448A-71
26	38.8	4.8	1196	1	US-08-290-448A-71
27	38.8	4.8	1196	1	US-08-175-069A-71

28	38.8	4.8	1196	4	US-08-461-939B-71	Sequence 71, Appl
29	38.8	4.8	1196	4	US-08-461-939B-71	Sequence 71, Appl
30	36.6	4.5	1036	4	US-09-072-596-304	Sequence 304, App
31	35.2	4.4	1368	1	US-08-290-448A-79	Sequence 79, Appl
32	35.2	4.4	1368	1	US-08-290-448A-79	Sequence 79, Appl
33	35.2	4.4	1368	1	US-08-175-069A-79	Sequence 79, Appl
34	35.2	4.4	1368	4	US-08-461-939B-79	Sequence 79, Appl
35	35.2	4.4	1368	4	US-08-461-939B-79	Sequence 79, Appl
36	34	4.2	4403765	4	US-09-103-840A-2	Sequence 2, Appl1
37	34	4.2	4411529	4	US-09-103-840A-1	Sequence 1, Appl1
38	33.6	4.2	7218	1	US-08-232-463-14	Sequence 14, Appl
39	33	4.1	726	4	US-08-818-112-24	Sequence 24, Appl
40	33	4.1	726	4	US-08-818-111-24	Sequence 24, Appl
41	33	4.1	726	4	US-09-056-556-24	Sequence 24, Appl
42	33	4.1	726	4	US-09-072-596-24	Sequence 24, Appl
43	33	4.1	33529	4	US-09-144-085-3	Sequence 3, Appl1
44	33	4.1	4403765	4	US-09-103-840A-2	Sequence 2, Appl1
45	33	4.1	4411529	4	US-09-103-840A-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-467-023-94
Sequence 94, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 26..1126
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 89..1126
US-08-467-023-94

Query Match 6.9%; Score 55.6; DB 3; Length 1170;
Best Local Similarity 62.5%; Pred. No. 2,7e-07;
Matches 85; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 360 TCTGTGCGGTTGACGCAACCGATGACGAGCTGCTGGCGGTGCGACCTGATTGSCA 419
DB 73 TGTATCTTGTACTCTGATATATCCCATGACAGCTGCTGGAGAGAGATTGCACTGGGA 132
QY 420 TGTCAACAGAAAAAGCTGCTGACTGCGCATTTGGCTTTGGACGCAACGCMATANGTG 479
DB 133 TCAAAACAGATGAGAGCTCCAGACTGTGCTGTGGATTGGAAAGCTCCACCATGGAGG 192

QY 480 CCGGACGGGGAATTT 495
DB 193 CAAAGGAGAGATTTT 208

RESULT 2
US-08-467-023-1
Sequence 1, Application US/08467023
Patent No. 6090386

GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mel H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: CRYPTOMERIA JAPONICA

FEATURE:
NAME/KEY: CDS
LOCATION: 66..1187
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 129..1187
US-08-467-023-1

Query Match 6.8%; Score 55.2; DB 3; Length 1337;
Best Local Similarity 51.7%; Pred. No. 3.8e-07;
Matches 181; Conservative 0; Mismatches 159; Indels 10; Gaps 3;

QY 349 TCTCTGTATCTGTGTCGCTGACGCAACCCGATGACGACTGCTGGCGGTGCGAC 408
DB 102 TCTTTTGTATTGGATCTCTTCTGATTAATCCATTAACAGCTGCTGGAGGAGAC 161
QY 409 CCTGATGGCATGTACACAGAAAAAGCTGCTGACTGCGGATTTGGCTTTGGACGCAAC 468
DB 162 TCAAACTGGGCCCCAAATAGATGAGAGCTGCAAGATTGTGAGTGGCTTCGGAAGCTCC 221
QY 469 GCNATANGTGGCCGCGAGGGAATTTGTTGTTGACAGACTCCGGGACNATGATCC 528
DB 222 ACCATGGGAGGCAAGGAGGAG-ATCTTTATAGGCTCAGCACTCAGATGACGA----CC 276
QY 529 CCGTGAATCTCGCCGCGGAGCACTTANATACCCGTCNCCANANGAATGGCCCTCT 588
DB 277 CTGTGAATCTGACACGAGAACTGTGCTATGAGAGAACCCGAGATGAGCCCTGTGGA 336
QY 589 GGGATCCCTTAAACNCNANANGAATCTCNCNANANGAAGAACTCMTTATGAACAG 648
DB 337 TAATTTCACTGGGAATATGAAATTAAGCTCAAAATGCTATGTAC-----ATTGCTGG 391
QY 649 CTTTANACNATGATGAGACNCGTGTCTGCTCCACATTTGCCAATGGCG 698
DB 392 GTATTAAGACTTTGATGAGGAGGAGCAAGATTATATTGGCAATGGCG 441

RESULT 3
US-08-467-023-96
Sequence 96, Application US/08467023
Patent No. 6090386

GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mel H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 1278 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 36..1145
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 99..1145
US-08-467-023-96

Query Match 6.7%; Score 54; DB 3; Length 1278;
Best Local Similarity 61.8%; Pred. No. 8.0e-07;
Matches 84; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 360 TCTGTCGTCGGTTCAGCAACCCGATCGACGACTGCGGCGGTGACCCCTGATTGGCA 419
DB 83 TGTACTGTTGCTCTGTGATTAATCCATAGACAGCTGCTGGAGAGAGATTCGAATCGGG 142
QY 420 TGTCAACAGAAAAAGCTGCTGACTGCGGCGATTGCTTTGGAGCCAAACGNATANGTGG 479
DB 143 TCAAAACAGAAATGAGAGCTGCGAGATTGCGCTGTGGGATTGGAGCTCCACCATGGAGG 202
QY 480 CCGGCGGCGGGAATTT 495
DB 203 CAAMGAGGAGATTTT 218

RESULT 4
US-08-290-448A-58
Sequence 58, Application US/08290448A
Patent No. 5676954
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rainier, Thorunn
APPLICANT: Kuo, Wei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragoras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1328
US-08-290-448A-58

Query Match 5.8%; Score 46.6; DB 1; Length 1328;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGCGTTTCAGGCAACCCGATCGACGACTGCTGGGCGGCGGACCCCTGATTGCAATGCA 424
DB 113 CATGTGAGACACACACATTAATAGACAGTCTGAGGTGCAAGCCGATTGGCGAATA 172
QY 425 ACAGAAAAAGCTGCTGACCTGCGGCGATTGCTTTGGAGCAACGCMATANGTGGCGCG 484
DB 173 ACCGACAAACGTTAGCCGATGCTGCGCAAGTTTGGCAAGGAAACCTACGGTGGAAC 232
QY 485 ACGGGGAAATTTGTTGTTGTGACAGACTCGGGGACNATGATCCCGTAATCTCGCCC 544
DB 233 ATGGGAT-----GTCACAGGCTCACACAGTGAAGAATGATGATGTTCAATYCA 285
QY 545 GGAACACTTANATACCCCGTCNTCCANGAAGTTGCCCCCTGTGGATCCCTTAAAC 604
DB 286 AAGAAGGACACTCCGTTTCTGCTGCGCCAAACAGGCCCTTGGATCATTTTAA 345
QY 605 NCNAAATGGAATCTCNCNANGAAGACTCNTTATGACAGCTTATTAACNATGAT 664
DB 346 ACAAAATATGTCATTCATTGTAATCAAGAGCTTGTGTAACAGGACAAACCATCAT 405
QY 665 GGACNCTGTCTCTGTCACATTTGCCAATGGCG 698
DB 406 GGCCGAGGGGTGAAGTTAAACATCGTTAACGCCG 439

RESULT 5
US-08-290-448A-58
Sequence 58, Application US/08290448A
Patent No. 5698204
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rainier, Thorunn
APPLICANT: Kuo, Wei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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1      APPLICATION NUMBER:  US/08/290.448A
2      FILING DATE:  August 15, 1994
3
4      PRIOR APPLICATION DATA:
5
6      APPLICATION NUMBER:  US 07/529,951
7      FILING DATE:  May 29, 1990
8      APPLICATION NUMBER:  US 07/325,365
9      FILING DATE:  March 17, 1989
10
11     ATTORNEY/AGENT INFORMATION:
12
13     NAME:  Amy E. Mandiagouras
14     REGISTRATION NUMBER:  36,207
15     REFERENCE/DOCKET NUMBER:  IM1-018CN
16
17     TELECOMMUNICATION INFORMATION:
18
19     TELEPHONE:  (617)227-7400
20     TELEFAX:  (617)227-5941
21
22     INFORMATION FOR SEQ ID NO:  58:
23
24     SEQUENCE CHARACTERISTICS:
25     LENGTH:  1328 base pairs
26     TYPE:  nucleic acid
27     STRANDEDNESS:  single
28     TOPOLOGY:  linear
29
30     MOLECULE TYPE:  CDNA
31
32     FEATURE:
33
34     NAME/KEY:  CDS
35     LOCATION:  1..1328
36
37     US-08-290-448A-58

```



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,939B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragoras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IM-018CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1328
US-08-461-939B-58

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	Query Match	5.8%:	Score 46.6:	DB 4:	Length 1328:	
	Best Local Similarity	46.7%:	Pred. No. 0.00016:			
	Matches 156:	Conservative 0:	Mismatches 171:	Indels 7:	Gaps 1:	
QY	365	CGTCCGGTTTCAGGACCCGATGCACGACTCTGGCGGTGGACCCTGATTGGCATGCCA	424			
Db	113	CATGTGAAGCACACAAACATTTATGACAAAGTCTGTGAGGTGCMAAGCCTATTGGCGCAATA	172			
QY	425	ACAGAAAAAACCTCGCTGACTGCGGCAATGGCTTTGACAGCAACGCNATANCTGGCCGCG	484			
Db	173	ACCGACAAGCGTTTAGCGGATTTGTGCCAAGGTTTTTGCAAAGGAACCTACGGTGGANAAC	232			
QY	485	ACGGGGAAATTTGTTGCTTTGTGACAGACTCCGGGACNATGATCCCCGGAATCTCGCCC	544			
Db	233	ATGGTGAAT-----GTCACACGGTCCACAGTGTATAAGAATGATGTGGCAATACCA	285			
QY	545	GGGAAACACTTANATACCCCGCTCNCTCCANANGAAGTTGGCCCTCTGGGATCCCTTTAAAC	604			
Db	286	AAAGAAAGGCACATCCGGTTTGCTGCTGCCAAAACAGGCCCTTGATCATTTTTPAAA	345			
QY	605	NCNAAATGGAATCTCNCTCNANNGGAAGAACTCNTATGACAGCTTTAANNACNATGCAT	664			
Db	346	AGAAATATGTGATTCATTATTAAATCACAAGCTTTGCTGTAAPACAGGCACAGCAATCGAT	405			
QY	665	GGACNCNGTGTCTCGTCCACATTTGCCAATGGCG	698			
Db	406	GGCGGAGGGGTGAAGTAACATCGTTAAACGCCG	439			

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US-08-464-000-58
: Sequence 58, Application US/08464000
: Patent No. 6335020
: GENERAL INFORMATION:
: APPLICANT: Rogers, Bruce
: APPLICANT: Klapper, David G.
: APPLICANT: Rafnar, Thorunn
: APPLICANT: Kuo, Mei-chang
: TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
: NUMBER OF SEQUENCES: 93
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD, LLP
: STREET: 60 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109-1675
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,000
: FILING DATE: 05-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/290,448
: FILING DATE: 15-AUG-1994
: APPLICATION NUMBER: US 07/529,951
: FILING DATE: 29-MAY-1990
: APPLICATION NUMBER: US 07/325,365
: FILING DATE: 17-MAR-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Amy E. Mandragouras
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: INI-018CN2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)227-5941
: INFORMATION FOR SEQ ID NO: 58:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1328 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1328
: US-08-464-000-58

```

[illegible]

DB 194 ACCGCAAGCGTTACCCGATTTGTGCCAAGGTTTTCGAAGGGAACCTACGGTGAAMAAC 253
QY 485 ACGGGGAATTTGTTGTTGTGACAGACTCCGGGACNMATGCCCGTAATCCTCCGCC 544
DB 254 ATGGGAT-----GTCTACACGGTCAACAGCTGATAAGATGATGATGTTGCAAAATCA 306
QY 545 GGGACACTTANATACCCGTCNTCCANGAAGTTGCCCTCTGGGATCCCTTTAAAC 604
DB 367 AAGAAGGCACACTCCGGTTGCTGCTGCCCAAAACAGGCCCTTGTGATCATTTTAA 366
QY 605 NCNAANTGGAATCTCNCNTCNANGAAGAACTNTATGACAGCTTTAANCMATCGAT 664
DB 367 AGAATATGATGATTCATTGTAATCAAGAGCTTGTGTAACAGGACAGACACATTCAT 426
QY 665 GGACMNCGTCTCTCTCCACATTCGCAATGCGG 698
DB 427 GGCCGAGGGGTGAAGTTAAACATCGTTAACGCCG 460

RESULT 11

US-08-175-069A-73
Sequence 73, Application US/08175069A
Patent No. 5776761

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mel-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175_069A
FILING DATE: December 29, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1323
US-08-175-069A-73

Query Match 5.8%; Score 46.6; DB 1; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CCGTGGCTTACGCAACCGATCGAGACTGCTGGGGGTCGACCCCTGATTTGCATGTCA 424
DB 134 CATGTGAGACACACAACTATATGACAACTGCTGAGAGTGCAAAAGCCGATTTGGCGAATA 193
QY 425 ACAGAAAAAGCTCGCTGACTGCGCATTTGCTTGGACGCAACCMATANTGTCGCCGG 484
DB 194 ACCGCAAGCGTTAGCCGATTTGTGCCCAAGGTTTTCGAAGGGAACCTACGGTGAAMAAC 253
QY 485 ACGGGGAATTTGTTGTTGTGACAGACTCCGGGACNMATGATCCCGTAATCCTCCGCC 544
DB 254 ATGGGAT-----GTCTACACGGTCAACAGCTGATAAGATGATGATGTTGCAAAATCA 306
QY 545 GGGACACTTANATACCCGTCNTCCANGAAGTTGCCCTCTGGGATCCCTTTAAAC 604
DB 307 AAGAAGGCACACTCCGGTTGCTGCTGCCCAAAACAGGCCCTTGTGATCATTTTAA 366
QY 605 NCNAANTGGAATCTCNCNTCNANGAAGAACTNTATGACAGCTTTAANCMATCGAT 664
DB 367 AGAATATGATGATTCATTGTAATCAAGAGCTTGTGTAACAGGACAGACACATTCAT 426
QY 665 GGACMNCGTCTCTCTCCACATTCGCAATGCGG 698
DB 427 GGCCGAGGGGTGAAGTTAAACATCGTTAACGCCG 460

RESULT 12

US-08-461-939B-73
Sequence 73, Application US/08461939B
Patent No. 635019

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mel-chang
TITLE OF INVENTION: Methods For Treating Sensitivity To A
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461_939B
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994

APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990

APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1323
US-08-461-9398-73

Query Match 5.8%; Score 46.6; DB 4; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTTCAGCAACCCGATGACGACCTGCTGGCGGTGCGACCCCTGATGGCATGTCA 424
DB 134 CATGTGAAGCACACACATTATGACAAAGCTGTGAGAGTGTCAAAAGCCGATTGGCGCAATA 193
QY 425 ACAGAAAAAGCTCGCTGACTGCGGCAATGCTTTGGACCAACGCNATANGTGGCCGCG 484
DB 194 ACCGACAGCGTTAGCCGATGTGCCAAGTTTGGAAAGGAACTAGCGTGGAAAC 253
QY 485 ACGGGGAATTTGCTGTGTGACAGACTCGGGGACNATGATCCCGTGAATCCTCGCCC 544
DB 254 ATGTGTAT-----GTCTACAGGTCACAGTGAATAGATGATGATGTTGCAAAATCCA 306
QY 545 GGGAACTTANATACCCCTCCTCCCAANGAAGTGGCCCTCTGGGATCCCTTTAAC 604
DB 307 AAGAAAGCACACTCGGTTGCTGCTGCCAAACAGCGCCCTGTGGATCATTTTTTAA 366
QY 605 NCNAAATGCAATCTCNCNANGAAGACTCNTTATGAACAGCTTTAANACNATGAT 664
DB 367 AGAAATATGTGTATTTGATTCATGATCAAGAGCTTGTGTAAACAGCCAGCAAGACCATGAT 426
QY 665 GGACNCGTGTCTCTCCACATTTGCCAATGGCG 698
DB 427 GGCCGAGGGGTGAAGTTAATCATCGTTAACGCCG 460

RESULT 13

US-08-464-000-73

Sequence 73, Application US/08464000

Patent No. 6335020

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce

APPLICANT: Klapper, David G.

APPLICANT: Rainier, Thorun

APPLICANT: Kuo, Wei-chang

TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHYE & COCKFIELD, LLP

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,000

FILING DATE: 05-JUN-1995

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/290,448

FILING DATE: 15-AUG-1994

APPLICATION NUMBER: US 07/529,951

FILING DATE: 28-MAY-1990

APPLICATION NUMBER: US 07/325,365

FILING DATE: 17-MAR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMT-018CN2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SRO ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

NAME/KEY: CDS
LOCATION: 1..1323
US-08-464-000-73

Query Match 5.8%; Score 46.6; DB 4; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTTCAGCAACCCGATGACGACCTGCTGGCGGTGCGACCCCTGATGGCATGTCA 424
DB 134 CATGTGAAGCACACACATTATGACAAAGCTGTGAGAGTGTCAAAAGCCGATTGGCGCAATA 193
QY 425 ACAGAAAAAGCTCGCTGACTGCGGCAATGCTTTGGACCAACGCNATANGTGGCCGCG 484
DB 194 ACCGACAGCGTTAGCCGATGTGCCAAGTTTGGAAAGGAACTAGCGTGGAAAC 253
QY 485 ACGGGGAATTTGCTGTGTGACAGACTCGGGGACNATGATCCCGTGAATCCTCGCCC 544
DB 254 ATGTGTAT-----GTCTACAGGTCACAGTGAATAGATGATGATGTTGCAAAATCCA 306
QY 545 GGGAACTTANATACCCCTCCTCCCAANGAAGTGGCCCTCTGGGATCCCTTTAAC 604
DB 307 AAGAAAGCACACTCGGTTGCTGCTGCCAAACAGCGCCCTGTGGATCATTTTTTAA 366
QY 605 NCNAAATGCAATCTCNCNANGAAGACTCNTTATGAACAGCTTTAANACNATGAT 664
DB 367 AGAAATATGTGTATTTGATTCATGATCAAGAGCTTGTGTAAACAGCCAGCAAGACCATGAT 426
QY 665 GGACNCGTGTCTCTCCACATTTGCCAATGGCG 698
DB 427 GGCCGAGGGGTGAAGTTAATCATCGTTAACGCCG 460

RESULT 14

US-08-232-463-14

Sequence 14, Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.

APPLICANT: SCHEIFLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463

FILING DATE:

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313

FILING DATE:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 12:40:30 ; Search time 123 Seconds

(without alignments)
9615.824 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806

Sequence: 1 TGTCTCTCTCTGATCACA.....TCCCTCTCTCTATGATNG 806

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published_Applications_MA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PC7_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/1/pubpna/PC7S_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	778	96.5	806	10	US-09-966-881-13 Sequence 13, Appl
2	543.8	67.5	727	10	US-09-966-881-16 Sequence 16, Appl
3	536	66.5	724	10	US-09-966-881-18 Sequence 18, Appl
4	142.8	17.7	842	10	US-09-966-881-17 Sequence 17, Appl
5	134.6	16.7	687	10	US-09-966-881-14 Sequence 14, Appl
6	124.2	15.4	1116	9	US-09-938-842A-1004 Sequence 1004, Ap
7	110.4	13.7	1215	9	US-09-938-842A-58 Sequence 58, Appl
8	93.4	11.6	460	10	US-09-770-444-439 Sequence 439, App
9	93	11.5	479	10	US-09-924-035A-174 Sequence 174, App
10	74.4	9.2	1629	9	US-09-938-842A-1766 Sequence 1766, Ap
11	68.4	8.5	277	10	US-09-923-876-4484 Sequence 4484, Ap
12	64.4	8.0	1185	9	US-09-938-842A-809 Sequence 809, App
13	56.2	7.0	388	10	US-09-878-574-3663 Sequence 3663, Ap
14	43.6	5.4	741	10	US-09-966-881-15 Sequence 15, Appl
15	41	5.1	1137	10	US-09-828-505-3 Sequence 3, Appl
16	37.6	4.7	481	9	US-09-918-995-25 Sequence 25, Appl
17	37.4	4.6	708	9	US-10-123-135-298 Sequence 298, App
18	35.6	4.4	360	10	US-09-864-761-27334 Sequence 27334, A
19	35.6	4.4	496	10	US-09-864-761-10689 Sequence 10689, A

20	35.2	4.4	594	9	US-10-123-155-10	Sequence 10, Appl
21	35.2	4.4	15425	9	US-10-091-504-1654	Sequence 1654, Ap
22	35.2	4.4	15425	10	US-09-764-869-1654	Sequence 1654, Ap
23	34.8	4.3	451	9	US-10-123-155-126	Sequence 126, App
24	34.4	4.3	1732	10	US-09-789-561-21	Sequence 21, Appl
25	34.2	4.2	4100	9	US-09-373-658-29	Sequence 29, Appl
26	34	4.2	2396	9	US-10-098-841-96	Sequence 96, Appl
27	34	4.2	2663	9	US-10-098-841-97	Sequence 97, Appl
28	34	4.2	4332	9	US-09-764-891-5756	Sequence 5756, Ap
29	34	4.2	7149	9	US-10-196-935A-1	Sequence 1, Appl
30	34	4.2	14155	9	US-10-108-603A-102	Sequence 102, App
31	33.8	4.2	724	9	US-10-123-155-60	Sequence 60, Appl
32	33.8	4.2	1049	9	US-10-123-155-358	Sequence 358, App
33	33.4	4.1	437	10	US-09-964-992A-4	Sequence 12835, A
34	33.4	4.1	671	9	US-10-184-634-346	Sequence 346, App
35	33.4	4.1	671	9	US-10-184-634-346	Sequence 346, App
36	33.4	4.1	2380	9	US-09-964-992A-4	Sequence 4, Appl
37	33.2	4.1	407	10	US-09-878-574-4048	Sequence 4048, Ap
38	33	4.1	519	9	US-10-123-155-210	Sequence 210, App
39	32.8	4.1	638	9	US-10-150-762-1	Sequence 1, Appl
40	32.8	4.1	661	9	US-10-121-988-34	Sequence 34, Appl
41	32.8	4.1	661	10	US-09-894-998-34	Sequence 34, Appl
42	32.8	4.1	1064	10	US-09-804-682-29	Sequence 29, Appl
43	32.8	4.1	2481	9	US-10-121-988-35	Sequence 35, Appl
44	32.8	4.1	2481	9	US-10-121-988-35	Sequence 35, Appl
45	32.8	4.1	2481	10	US-09-894-998-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-966-881-13
Sequence 13, Application US/09966881
Patent No. US20020120960A1
GENERAL INFORMATION:
APPLICANT: Seymour, Graham
Baird, Collin
Medina-Sanchez, Rosybel
TITLE OF INVENTION: Genetic control of Fruit Ripening
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSER: Zeneca Ag Products Inc.
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,881
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/242,860
FILING DATE: 29-Mar-1999
APPLICATION NUMBER: GB 9618862.8
FILING DATE: 10-Sep-1996
APPLICATION NUMBER: GB 9708366.1
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: PCT/GB97/02424
FILING DATE: 08-Sep-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschultz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: SEE 50183/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 806 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 CLONE: U-068

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-09-966-881-13

Query Match

Best Local Similarity 96.5%; Score 778; DB 10; Length 806;
 Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TGTTCCTCCTTGATCATCTTTTGTCTGGGAAACGTGAGAGGTGAGAGGCGG 60
DB 1 TGTTCCTCCTTGATCATCTTTTGTCTGGGAAACGTGAGAGGTGAGAGGCGG 60
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DB 61 GCATGACGGCGGTTTAAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CTGCTTTTGAACGAGAGTCTGGGGGTGATTTGAAGCAGAGGTCTCTCTCTCT 180
DB 121 CTGCTTTTGAACGAGAGTCTGGGGGTGATTTGAAGCAGAGGTCTCTCTCTCT 180
QY 181 GGGGAGCATCGGCGGAGGAGCTTGAGAGGCGCTCCGCGAAGCGACGAGCGGATCT 240
DB 181 GGGGAGCATCGGCGGAGGAGCTTGAGAGGCGCTCCGCGAAGCGACGAGCGGATCT 240
QY 241 TCCTTGAAGAGAGGCGTGTAAACCGGCGAGAGACCGCAGTCAAGACCCGAGAG 300
DB 241 TCCTTGAAGAGAGGCGTGTAAACCGGCGAGAGACCGCAGTCAAGACCCGAGAG 300
QY 301 GTTGTCTCGAGCTCTGATGACCATTAATCAACAGACGCGCTGGAGATCTTTGGTAT 360
DB 301 GTTGTCTCGAGCTCTGATGACCATTAATCAACAGACGCGCTGGAGATCTTTGGTAT 360
QY 361 CTGTCTGCGGTTTCAGGCAACCGCATGACGAGTCTGGGGGTGCGACCTGATTTG 420
DB 361 CTGTCTGCGGTTTCAGGCAACCGCATGACGAGTCTGGGGGTGCGACCTGATTTG 420
QY 421 GTCAACAGAAAAAAGCTGCTGACTGAGCGGCGGATTTGGAGCAACGCMATANGTGC 480
DB 421 GTCAACAGAAAAAAGCTGCTGACTGAGCGGCGGATTTGGAGCAACGCMATANGTGC 480
QY 481 CGGAGCGGGAATTTGTCTGTGTGACAGACTCCGGGAGCMATGATCCCGTAATCTTC 540
DB 481 CGGAGCGGGAATTTGTCTGTGTGACAGACTCCGGGAGCMATGATCCCGTAATCTTC 540
QY 541 GCCCGGGAACACTTANATACCCGCTNTCCANGAAGTTGCCCTCTGGGATCCCTTT 600
DB 541 GCCCGGGAACACTTANATACCCGCTNTCCANGAAGTTGCCCTCTGGGATCCCTTT 600
QY 601 AAACNCAANTGAAATCTCNCNANANGAAGAACTCCTTATGACAGCTTTAANCMAT 660
DB 601 AAACNCAANTGAAATCTCNCNANANGAAGAACTCCTTATGACAGCTTTAANCMAT 660
QY 661 CGATGACNNGTCTCTGTCACATGTCGATGCGGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 CGATGACNNGTCTCTGTCACATGTCGATGCGGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 TCCCAACNCTCTCTTCNNTNGCCTCNCCTCCCAATGCAACCCGCGGAATTTCTNGT 780
DB 721 TCCCAACNCTCTCTTCNNTNGCCTCNCCTCCCAATGCAACCCGCGGAATTTCTNGT 780
QY 781 CCCCNCTCCCTCTCTCTATGATNG 806
DB 781 CCCCNCTCCCTCTCTCTATGATNG 806

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RESULT 2

US-09-966-881-16

Sequence 16, Application US/09966881
 Patent No. US20020120960A1

GENERAL INFORMATION:

APPLICANT: Seymour, Graham
 Bird, Colin

Medina-Suarez, Rosybel

TITLE OF INVENTION: Genetic control of Fruit Ripening

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zeneca Ag Products Inc.

STREET: 1800 Concord Pike

CITY: Wilmington

STATE: DE

COUNTRY: USA

ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/966,881

FILING DATE: 28-Sep-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/242,860

FILING DATE: 29-Mar-1999

APPLICATION NUMBER: GB 9618862.8

FILING DATE: 10-Sep-1996

APPLICATION NUMBER: GB 9708366.1

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: PCT/GB97/02424

FILING DATE: 08-Sep-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hohenschutz, Liza D.

REGISTRATION NUMBER: 33,712

REFERENCE/DOCKET NUMBER: SEE 50183/JST

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 886-1699

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 727 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: U-089

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-966-881-16

Query Match

Best Local Similarity 67.5%; Score 543.8; DB 10; Length 727;
 Matches 628; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

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QY 2 GTTCTCTCTCGATCATCTTTTGTCTGGGAAACGTGAGAGGTGAGAGGCGG 61
DB 2 GTTCTCTCTCGATCATCTTTTGTCTGGGAAACGTGAGAGGTGAGAGGCGG 61
QY 8 GTTCTCTCTCGATCATCTTTTGTCTGGGAAACGTGAGAGGTGAGAGGCGG 67
DB 8 GTTCTCTCTCGATCATCTTTTGTCTGGGAAACGTGAGAGGTGAGAGGCGG 67
QY 62 CAATGACGGCGGTTTAAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 121
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QY 122 TGTGTTTGAACGAGAGTCTGGGGGTGATTTGAAGCAGAGGTCTCTGCTGAGGAATG 181
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QY 182 GCGGACATCGCGAGAGGCTTTGAGAGGCTTCGCGAAGCGGACGAGCGCGGATGCTT 241
DB 182 GCGGACATCGCGAGAGGCTTTGAGAGGCTTCGCGAAGCGGACGAGCGCGGATGCTT 241
QY 242 CCTTGAAGAGAGGCGCTTAAACCGGCGAGAGCCGCGATGACGACCCGAGGAGG 301
DB 242 CCTTGAAGAGAGGCGCTTAAACCGGCGAGAGCCGCGATGACGACCCGAGGAGG 301

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Oy 388 ATGAGAGACTGCGCGCGGCGGCGACCGCTATTGGCATGTGCACACAGAAAAAGCTGGCTGAC 444
 Db 200 ATGAGAGACTGCGCGGCGGCGGCGACCGCTATTGGCATGTGCACACAGAAAAAGCTGGCTGAC 259
 Oy 445 TGGCGATTGGCGTTTGGAGCGCAAGCANNATANGGCGCGGAGGAGAAATTTGTTGCGTGT 504
 Db 260 TGGCGCATGGGCGTTGCGGAGAAAGCGGATGGGGGCGAGGAGCGCG - AGATATACGTGCT 318
 Oy 505 GACAGACTCGGGGAGCANNATATCCCGGTGAATCCTCGCGCGGGAACACTTANATATCCCG 564
 Db 319 GACCGAGACATGGCGAGACNACNA - CCGCGTCAATCCGAACCGGGGACGCGTGGTAGCGCG 377
 Oy 565 TCCTCCAAAGAAAGTTGCCCGCTCTGGGATCCCGTTTAACMCNANATGGAAATTCCTC 624
 Db 378 TCCTCCAAAGAGGAGCGCGCTGT - GGATCATCTTTCGAAGCGCGACATGTGTCTCAAGTC 434
 Oy 625 NANGAGAGAAGCTCCTTATGAA - CAGCTTTAANACNATCGATGGAGCNCNGTCTCGTGC 682
 Db 435 AAGGAGAGAGCTCATCATCAATAACCTCCACANNAGACATCGACGGCCGGGGGCCGACGCTC 494
 Oy 683 CACATTGCCAATGGCGCGCTGCTCAACANCAATTTCTCCCAACATCTTCTCCNTG 742
 Db 495 CACATCTCGGGGGGCGGCGTCAACACAC - AGTNGTNCNCAATCATCATCCAGCG 552
 Oy 743 CCTCCMCCTCCCAATGACCAACCCCGGG 770
 Db 553 GCGTCCAGTTCCACNNAATGACNAGG 580

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RESULT 6
US-09-938-842A-1004
; Sequence 1004, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT00-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1004
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1004

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Query Match	15.4%	Score 124.2	DB 9	Length 1116
Best Local Similarity	60.2%	Pred. No. 2.7e-30		
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QY	319	ATGACCATTAATCAACAGCAGCAGCGCTCGCAGATCTCTTGTTATATCTCGTCGGCGGTCAGGC	378	
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QY	379	AACCCGATTCGACGACTGCTGGCGTGCAGCCCTGATTGGCATGTCACAGAAAAAAGCTC	438	
Db	61	AACCCATTCGACGAGTTGTTGGCGAATGTACCCCAATTTGGCAACAGAACCTTAAGCCCTA	120	
QY	439	GCTACACGCGGCATTGGCTTTGGACGCAACGCNMTANSTGGCCGCGAGACGGGAATTTGTT	498	
Db	121	GGGATATTCGATATTCGATTTGGAAAGAAACCGATCCGGTGTCTCGATGGAGCA-TTCTA	179	

Oy	CGTTTGACACGACTCCGGGGACNANGATCCCCGTAAATCMTGCCCGGGAACACTTANAT	558	
	499		
	180	CGTAGTACTAGACCCCAAGACGACAAAT-CCGGTTAAACCTTAGACGGGACCTTACGTC	238
Db			
Oy	559	ACCCGCGTCNTCCAANGAAGTTGCGCCCTCTGGGATCCCTTTAAACNMANNTGGAATC	618
	239	ACGCCGATGACAAAG-----ACCGAACACTATGATCGTTTCCAAGGTGACATGGTAT	293
Db			
Oy	619	TCNCTNANGAAGAACCTNTTATGACAGCTTTAANCMNTCGATGAGACNCGTGTCT	678
	294	TCAGCTAAACAAACAGACCTTATCGTTAACAGTTTCAAAACGATCATGACGTGGCGCAA	353
Db			
Oy	679	CGTCCACATTTGCCAATGGGCGCTCGNTGATCCACNCCAATTT	718
	354	CGTTCACATATGCTAACGCGTGGTTGCATCACGATTAGTTT	393
Db			

RESULT 7
US-09-938-842A-58
Sequence 58, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kieps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPT00-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 58
LENGTH: 1215
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-58

	Query Match	13.7%	Score 110.4	DB 9	Length 1215	
	Best Local Similarity	59.0%	Pred. No. 9.1e-26			
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Db	147 TAGGTACTCTCATGTAAGACCCGGTAACCATAATGAGACTGTTGGGGTTGTGAACCTC	206				
OY	413 ATTGGCATGTCAACAGAAAAGCCGCTGACTGGCGGATTGGCTTTGGAGCAACGGNA	472				
Db	207 ACTGGGACAACACCGCTCAACGTCGCTGACTGGCCATTGGATTGGCAAAAGGCA	266				
OY	473 TANGTGGCGCGAGCGGGGATTTGTTGCTGTGAGACAGACTCGGGGACNATGATCCCGT	532				
Db	267 TCGETGGCGGTGAC -GGTCGATCTACGTGGTCACCGACTAGGAAAGA -CAACCCAGT	324				
OY	533 GAATCTGCGCCGGGACACTTANATATACCCGCTCTTCACANAAGATTCGCCCTTGAGA	592				
Db	325 TAGCCCCAAGCCCGGAACTTTAAGACACGCCGTGTC-----AAGACAGCCACTCTGGA	380				
OY	593 TCCCCTTTAAACNCNANTGGAATCTCTCNCTCNANGAAGAAGCTCNTATGAACGCTTT	652				
Db	381 TCATCTTCCAAGAGACATGACGATTCAGCTCAA -GAAAGACTATCATGAACATCTTC	439				
OY	653 AANACNTGATGAGCANCGTGTCTCGTCACATTTGCCAATGGCGCCTGCNTCACANC	712				
Db	440 AAGACCATGCATGGCGCGTGGTGCTTCGTTACACATCTGTGGTGGGCCCTTGATTAAGCATC	499				
OY	713 CAATTTCNTCCCAACACTTCTTCCTCNNTNGCCTCCNCTCCCAAT	757				

142,	CONSERVATIVE	0,	MISMATCHES	11,	INVERTS	1,	GAPS
MATCHES							

US-09-828-505-3

Query Match 5.1%; Score 41; DB 10; Length 1137;
 Best Local Similarity 56.5%; Pred. No. 0.0048;
 Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY	365	CCTGGGTTCAAGCAACCCGATCGACGCTGTGGGGTGCACCTGATTGGCATGTCA	424
Db	74	CCTCGGAGCTTACACATTATTGATGGCTGTGGAGGGGGAAGCAGATTGGCCGAAA	133
QY	425	ACAGAAAAAGCTCGCTGACTGCGGCAATTGGCTTTGGACGCAACGCNATANGTGGCCGCG	484
Db	134	ACCGCAGGCGCACTGGCTGACTGTGCCCAAGGTTTGGCAAGGTACCGTGGTGGCAAGG	193
QY	485	ACGGGGAATT 495	
Db	194	ACGGAGACATT 204	

Search completed: June 19, 2003, 13:34:04
 Job time : 124 secs

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